



# **STIC Search Report**

## **Biotech-Chem Library**

STIC Database Tracking Number: 133469

TO: James Schultz  
Location: REM/2D18/2C18  
Art Unit: 1635  
Thursday, September 23, 2004

Case Serial Number: 09/227881

From: David Schreiber  
Location: Biotech-Chem Library  
Remsen E01A61  
Phone: 272-2526

david.schreiber@uspto.gov

### Search Notes



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Schreiber, David

133469

**From:** Schultz, James  
**Sent:** Tuesday, September 14, 2004 11:30 AM  
**To:** Schreiber, David  
**Subject:** RE: Seq Search 09/227,881

OK, just run it on the full length SEQ Id NO:3.  
thanks,  
Doug

-----Original Message-----

**From:** Schreiber, David  
**Sent:** Tuesday, September 14, 2004 11:21 AM  
**To:** Schultz, James  
**Subject:** RE: Seq Search 09/227,881

Doug,

Seq3 is only 6169 residues long. It doesn't make sense to run a separate search for the fragment in score over length when the fragment is so close in length to the full length sequence.

David Schreiber, Ph.D.  
Scientific and Technical Information Center  
Biotech/Chem Library  
Old address and phone:  
CM1-6A03  
703-308-4292  
New address and phone:  
Remsen E01A61  
571-272-2526

-----Original Message-----

**From:** Schultz, James  
**Sent:** Tuesday, September 14, 2004 11:16 AM  
**To:** Schreiber, David  
**Subject:** Seq Search 09/227,881

Hi David,

Could you please run a score over length nucleotide sequence search on nucleotides 1 through 5271, and also on the full length of SEQ ID NO:3 in the above entitled case, which returns hits between 12 and 250 nucleotides long? Please transfer in as many hits as possible, but only include those that are 100% identical to the target. Please include the interference databases as well.

Thanks,  
Doug Schultz

*James Douglas Schultz, PhD*  
AU 1635 (Biotechnology)  
Patent Examiner  
United States Patent and Trademark Office  
(Office) REM 2D18  
(Mail) REM 2C18  
(571) 272-0763

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 09:55:27; Search time 7 Seconds

(without alignments)  
3.592 Million cell updates/sec

Title: US-09-227-881-3

Percent score: 6169  
Sequence: 1 atcttgcgtcagttacctc.....cttgcccccctcatgctcag 6169

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 0.5

Searched: 76 seqs, 2038 residues

Total number of hits satisfying chosen parameters: 152

Minimum DB seq length: 12

Maximum DB seq length: 250

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 77 summaries

Database: rng3.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	3.7	227	1	AAA57515
2	29	0.5	29	1	AAZ37976
3	28	0.5	28	1	AAQ33645
4	28	0.5	28	1	AAQ34161
5	28	0.5	28	1	AAQ34035
6	28	0.5	28	1	AA66102
7	27	0.4	27	1	AAQ34044
8	27	0.4	27	1	AAQ33678
9	27	0.4	27	1	AAQ33804
10	27	0.4	27	1	AAQ34181
11	27	0.4	27	1	AAQ34012
12	27	0.4	27	1	AAQ34143
13	27	0.4	27	1	AAQ33951
14	27	0.4	27	1	AA65733
15	27	0.4	27	1	AAH24300
16	27	0.4	27	1	AAH46017
17	27	0.4	27	1	AAH46001
18	27	0.4	27	1	AAH46005
19	27	0.4	27	1	AA660473
20	26	0.4	26	1	AAQ34083
21	26	0.4	26	1	AAQ33684
22	26	0.4	26	1	AAQ33704
23	26	0.4	26	1	AAQ33831
24	26	0.4	26	1	AAQ33837
25	26	0.4	26	1	AAQ36250
26	25	0.4	25	1	AAQ33918
27	25	0.4	25	1	AAQ33642
28	25	0.4	25	1	AAQ33962
29	25	0.4	25	1	AAQ33861
30	25	0.4	25	1	AAH40163
31	25	0.4	25	1	AAH38303
32	25	0.4	25	1	AAH38303
33	25	0.4	25	1	ABA96251

34	24	0.4	24	1	AAQ33986	Microsatellite seq
35	24	0.4	24	1	AAQ34158	Sequence of a micr
36	24	0.4	24	1	AAQ33909	Microsatellite seq
37	24	0.4	24	1	AAQ34065	Microsatellite seq
38	24	0.4	24	1	AAQ34024	Microsatellite seq
39	24	0.4	24	1	AAQ33707	Microsatellite seq
40	24	0.4	24	1	AA66095	Repeat sequence fo
41	24	0.4	24	1	AAH46015	Synthetic oligonuc
42	24	0.4	24	1	AAH46016	Synthetic oligonuc
43	24	0.4	24	1	AA69862	Immunostimulatory
44	24	0.4	24	1	AB678584	Arginogenesis inhib
45	24	0.4	24	1	ABZ70110	Human RNA polymera
46	24	0.4	24	1	ACH03377	Immunostimulatory
47	24	0.4	24	1	AD337264	Immunostimulatory
48	24	0.4	24	1	AAQ33863	Microsatellite seq
49	23	0.4	23	1	AAQ33773	Microsatellite seq
50	23	0.4	23	1	AAQ33885	Microsatellite seq
51	23	0.4	23	1	AA66105	Repeat sequence fo
52	23	0.4	23	1	AA660472	Oligonucleotide cl
53	22.4	0.4	227	1	AAA57515	Trabecular meshwor
54	22	0.4	22	1	AAQ33810	Microsatellite seq
55	22	0.4	22	1	AAQ33675	Microsatellite seq
56	22	0.4	22	1	AAQ34038	Microsatellite seq
57	22	0.4	22	1	AAQ34080	Microsatellite seq
58	22	0.4	22	1	AAQ33991	Microsatellite seq
59	22	0.4	22	1	AAQ83952	Oligonucleotide cl
60	22	0.4	22	1	AA65727	Repeat sequence fr
61	22	0.4	22	1	AA64448	SSR motif #8. Uni
62	22	0.3	22	1	AAQ33891	Microsatellite seq
63	21	0.3	21	1	AAQ34015	Microsatellite seq
64	21	0.3	21	1	AAQ33879	Microsatellite seq
65	21	0.3	21	1	AA650296	Oligonucleotide RT
66	21	0.3	21	1	AA655738	Repeat sequence fr
67	21	0.3	21	1	AA651377	Human TIGR PCR pri
68	21	0.3	21	1	AA651373	Human TIGR PCR pri
69	21	0.3	21	1	AA657495	Primer used for SS
70	21	0.3	21	1	AA657491	Synthetic oligonuc
71	21	0.3	21	1	AAH46013	Synthetic oligonuc
72	21	0.3	21	1	AAH46014	Immunostimulatory
73	21	0.3	21	1	AA69702	Arginogenesis inhib
74	21	0.3	21	1	AB678423	IFNARI forward PCR
75	21	0.3	21	1	AC664053	Immunostimulatory
76	21	0.3	21	1	ACH03241	Immunostimulatory
77	21	0.3	21	1	ADB37204	Immunostimulatory

#### ALIGNMENTS

RESULT 1	
AAA57515	
ID AAA57515 standard; DNA; 227 BP.	
XX	
AC AAA57515;	
XX	
DT 20-OCT-2000 (first entry)	
XX	
DE Trabecular meshwork inducible glucocorticoid receptor gene fragment.	
XX	
KW TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;	
KM glucoma; steroid sensitivity; progressive ocular hypertension;	
XX	
OS Homo sapiens.	
XX	
PN W0200042220-A1.	
XX	
PD 20-JUL-2000.	
XX	
PF 11-JAN-2000; 2000NC-US000559.	
XX	
PR 11-JAN-1999; 99US-00227881.	
PR 07-MAY-1999; 99US-00306828.	

XX (REGC ) UNIV CALIFORNIA.  
 PA  
 XX  
 PI Nguyen TD, Polansky JR, Chen P, Chen H;  
 XX  
 XX WPI; 2000-491060/43.  
 DR  
 XX  
 PT Diagnosis, prognosis and treatment of glaucoma, based on detecting  
 PT specific polymorphisms in the promoter of the trabecular meshwork  
 PT inducible glucocorticoid receptor gene.  
 XX  
 PS Claim 90; Page 113; 122pp; English.  
 CC The present sequence represents a fragment of a TIGR (trabecular meshwork  
 CC inducible glucocorticoid receptor) gene. The specification describes a  
 CC method for the diagnosis, prognosis and treatment of glaucoma, based on  
 CC detecting specific polymorphisms in the promoter of the TIGR gene. The  
 CC method is used for diagnosis and prognosis of glaucoma (of all types),  
 CC steroid sensitivity and progressive ocular hypertension that leads to  
 CC loss of vision. Glaucoma can be treated by administering an agent that  
 CC binds to cis-acting elements within the TIGR promoter. The TIGR promoter  
 CC (or other regulatory regions) can be used to express homologous or  
 CC heterologous genes, particularly for tissue-specific expression of  
 CC therapeutic transgenes for treating glaucoma, also to generate transgenic  
 CC animals and in screening for compounds (specific modulators) with  
 CC diagnostic or therapeutic potential. Fragments of the TIGR sequence can  
 CC be used as amplification primers or probes, e.g. for isolating related  
 CC sequences in non-human animals  
 XX  
 SQ Sequence 227 BP; 57 A; 61 C; 53 G; 56 T; 0 U; 0 Other;  
 XX  
 Query Match 3.7%; Score 227; DB 1; Length 227;  
 Best Local Similarity 100.0%; Pred. No. 1.9e-15;  
 Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5045 AACTATTATGCGGTATGCGTCAATTAATGCGATGTTCTTTTAAAGAACTCCAAA 5104  
 DB 1 AACTATTATGCGGTATGCGTCAATTAATGCGATGTTCTTTTAAAGAACTCCAAA 60  
 QY 5105 CAGACTCTGGAAGGTATTTCTTAAGAATCTGCTGCGACGGTGAAGGCAACCCCTG 5164  
 DB 61 CAGACTCTGGAAGGTATTTCTTAAGAATCTGCTGCGACGGTGAAGGCAACCCCTG 120  
 QY 5165 TGGACAGCCCAACCAAGCTCACTGCGACCTCTGTCTTCCCAATGAAGGCTGCTC 5224  
 DB 121 TGGACAGCCCAACCAAGCTCACTGCGACCTCTGTCTTCCCAATGAAGGCTGCTC 180  
 QY 5225 CCAGATATATTAACCTCTCTGAGCTCGGCGAAGACCGCAAGG 5271  
 DB 181 CCAGATATATTAACCTCTCTGAGCTCGGCGAAGACCGCAAGG 227

RESULT 2  
 AA237976  
 ID AA237976 standard; DNA; 29 BP.  
 AC AA237976;  
 XX  
 DT 07-FEB-2000 (first entry)  
 XX  
 DE GLC1A coding sequence fragment (basepair 344-372).  
 XX  
 XX GLC1A gene; human, ss.  
 KW  
 XX Homo sapiens.  
 OS  
 XX  
 PN MO9951779-A2.  
 XX  
 PD 14-OCT-1999.  
 XX  
 PF 07-APR-1999; 99WO-US007671.  
 XX

PR 07-APR-1999; 98US-00056285.  
 XX  
 PA (IOWA ) UNIV IOWA RES FOUND.  
 XX  
 PI Stone EM, Sheffield VC, Alward WM, Fingert J;  
 XX  
 XX WPI; 2000-022956/02.  
 DR  
 XX  
 PT Determination of a predisposition to glaucoma by analysing mutations in  
 PT the GLC1A gene.  
 XX  
 PS Disclosure; Page 14; 137pp; English.  
 CC The invention relates to a method for the determination of a  
 CC predisposition to glaucoma. The method comprises amplifying a GLC1A gene  
 CC with a primer pair selected from the sequences shown in AA237981-238008.  
 CC The primers are used to determine whether a subject has or has the  
 CC potential to develop primary open wide angle glaucoma. The present  
 CC sequence represents the human GLC1A coding sequence fragment (basepair  
 CC 344-372), which is not included in the TIGR sequence  
 XX  
 SQ Sequence 29 BP; 5 A; 7 C; 14 G; 3 T; 0 U; 0 Other;  
 XX  
 Query Match 0.5%; Score 29; DB 1; Length 29;  
 Best Local Similarity 100.0%; Pred. No. 11;  
 Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 5680 AGGGGCTGCAAGAGGAGCTGGGCAACCTG 5708  
 DB 1 AGGGGCTGCAAGAGGAGCTGGGCAACCTG 29

RESULT 3  
 AAQ33645  
 ID AAQ33645 standard; DNA; 28 BP.  
 AC AAQ33645;  
 XX  
 DT 25-MAR-2003 (revised)  
 DT 02-FEB-1993 (first entry)  
 XX  
 DE Microsatellite sequence from clone MTG73.  
 XX  
 XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
 KW genetic mapping; traits; amplification; ss.  
 XX  
 OS Bos taurus.  
 PN WO9213102-A1.  
 XX  
 PD 06-AUG-1992.  
 XX  
 PF 15-JAN-1992; 92WO-US000340.  
 XX  
 PR 15-JAN-1991; 91US-00642342.  
 XX  
 PA (GENM-) GENMARK.  
 XX  
 PI Georges M, Massey JM;  
 XX  
 DR WPI; 1992-284684/34.  
 XX  
 PT Polymorphic bovine DNA markers - used in genetic identification, gene  
 PT mapping, and selective breeding.  
 PS Table 7; Page 187; 517pp; English.  
 CC The sequence is that of a bovine microsatellite sequence obtd. by  
 CC screening a library of bovine MboI DNA fragments of between 250 and 500  
 CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
 CC clones cross-hybridised. Assuming independent distribution of  
 CC microsatellites and MboI sites, the frequency of (76)n >9 microsatellites  
 CC in the bovine genome is estimated at >100, 000. The sequence information

for ca. 330 such bovine microsatellites is summarised in the CC specification and indexed herein (see below). The sequences upstream and CC downstream of the microsatellite sequence were used to generate the CC required PCR primers for in vitro amplification of the corresp. CC microsatellite (using the program OPRIPRM). The microsatellites may be CC used to identify individuals, for parentage testing, and in the genetic CC mapping of economic trait loci, or genes involved the determination of CC economically important traits esp. in cattle, to allow selective CC breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN CC field.)

XX Sequence 28 BP; 0 A; 0 C; 14 G; 14 T; 0 U; 0 Other;

SQ Query Match 0.5%; Score 28; DB 1; Length 28;  
Best Local Similarity 100.0%; Pred. No. 12;  
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

OY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 5023  
|||||  
Db 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 28

RESULT 4  
AAQ34161  
ID AAQ34161 standard; DNA; 28 BP.  
XX  
AC AAQ34161;  
XX  
DT 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)

DE Sequence of a microsatellite from clone TGA82.  
XX  
KW PCR: selection; primers; OPRIPRM; breeding; cattle; parentage;  
KM Genetic mapping; traits; amplification; ss.  
XX  
OS Bos taurus.  
XX  
PN WO921102-A1.  
XX  
PD 06-AUG-1992.  
XX  
PF 15-JAN-1992; 92WO-US000340.  
XX  
PR 15-JAN-1991; 91US-00642342.  
XX  
PA (GENM-) GENMARK.  
XX  
PI Georges M, Massey JM.  
DR WPI, 1992-284684/34.  
XX  
PT Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.  
XX  
PS Table 7; Page 395; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obt'd. by  
CC screening a library of bovine Mbcl DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and Mbcl sites, the frequency of (T6)n >9 microsatellites  
CC in the bovine genome is estimated at >100, 000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPRIPRM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved the determination of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)

[illegible]



[illegible]

PT mapping and selective breeding.

XX PS Table 7; Page 251; 517pp; English.

CC The sequence is that of a bovine microsatellite sequence obtd. by  
CC screening a library of bovine MbOI DNA fragments of between 250 and 500  
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50  
CC clones cross-hybridised. Assuming independent distribution of  
CC microsatellites and MbOI sites, the frequency of (76)n >9 microsatellites  
CC in the bovine genome is estimated at >100,000. The sequence information  
CC for ca. 230 such bovine microsatellites is summarised in the  
CC specification and indexed herein (see below). The sequences upstream and  
CC downstream of the microsatellite sequence were used to generate the  
CC required PCR primers for in vitro amplification of the corresp.  
CC microsatellite (using the program OPTIPRIM). The microsatellites may be  
CC used to identify individuals, for parentage testing, and in the genetic  
CC mapping of economic trait loci, or genes involved the determinism of  
CC economically important traits esp. in cattle, to allow selective  
CC breeding. See also AAQ31501-34437. (Updated on 25-MAR-2003 to correct PN  
CC field.)

XX SQ Sequence 27 BP; 0 A; 0 C; 13 G; 14 T; 0 U; 0 Other;

Query Match 0.4%; Score 27; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred.No. 14;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4997 TGAGTGTGAGTGTGAGTGTGAGTGTGT 5023 308  
Db 1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

RESULT 10  
AAQ34181  
ID AAQ34181 standard; DNA; 27 BP.

AC AAQ34181;  
XX 25-MAR-2003 (revised)  
DT 02-FEB-1993 (first entry)

DE Microsatellite sequence from clone TGLA98.

XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;  
KM genetic mapping; traits; amplification; ss.  
XX Bos taurus.  
OS  
XX WO9213102-A1.  
EN  
XX 06-AUG-1992.  
FD  
XX 15-JAN-1992; 92WO-US0000340.  
FE  
XX 15-JAN-1991; 91US-00642342.  
XR  
XX (GENM-) GENMARK.  
PA  
XX Georges M, Massey JM;  
X1 WPI; 1992-284684/34.  
DR  
XX Polymorphic bovine DNA markers - used in genetic identification, gene  
PT mapping, and selective breeding.

XX PS Table 7; Page 403; 517pp; English.

CC The sequence is a bovine microsatellite sequence obtd. by screening a  
CC library of bovine MbOI DNA fragments of between 250 and 500 bp with an  
CC (AC)15 and a (TC)15 oligonucleotide probe. One out of 50 clones cross-  
CC hybridised. Assuming independent distribution of microsatellites and MbOI  
CC sites, the frequency of (76)n >9 microsatellites in the bovine genome is  
CC estimated at >100,000. The sequence information for ca. 230 such bovine





[illegible][illegible]



[illegible][illegible]



[illegible][illegible]

[illegible][illegible]











[illegible]

XX	DE	Microsatellite sequence from clone TGLA444.
XX	KW	PCR; selection; primers; OPTIRIM; breeding; cattle; parentage;
XX	KM	genetic mapping; traits; amplification; ss.
XX	OS	Bos taurus.
XX	PN	MO9213102-A1.
PD	PD	06-AUG-1992..
XX	PF	15-JAN-1992; 92WO-US000340.
XX	PR	15-JAN-1991; 91US-00642342.
XX	PA	(GENM-) GENMARK.
XX	PI	Georges M, Massey JM;
XX	DR	WPI; 1992-284684/34.
XX	PT	Polymorphic bovine DNA markers - used in genetic identification; gene
XX	PS	mapping; and selective breeding.
XX	PS	Table 7; Page 357; 517pp; English.
CC	CC	The sequence is that of a bovine microsatellite sequence cbtd. by
CC	CC	screening a library of bovine MbOI DNA fragments of between 250 and 500
CC	CC	bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC	CC	clones cross-hybridised. Assuming independent distribution of
CC	CC	microsatellites and MbOI sites, the frequency of (76)n > 9 microsatellites
CC	CC	in the bovine genome is estimated at >100,000. The sequence information
CC	CC	for ca. 230 such bovine microsatellites is summarised in the
CC	CC	specification and indexed herein (see below). The sequences upstream and
CC	CC	downstream of the microsatellite sequence were used to generate the
CC	CC	required PCR primers for in vitro amplification of the corresp.
CC	CC	microsatellite (using the program OPTIRIM). The microsatellites may be
CC	CC	used to identify individuals, for percentage testing, and in the genetic
CC	CC	mapping of economic trait loci, or genes involved the determination of
CC	CC	economically important traits esp. in cattle, to allow selective
CC	CC	breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
SO	SO	field.)
XX	XX	Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;
XX	XX	Query Match 0.4%; Score 24; DB 1; Length 24;
XX	XX	Best Local Similarity 100.0%; Pred. No. 22;
XX	XX	Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	OY	4996 GTGTGCTGTGTGTGTGTGTGTGT 5019
DB	DB	
DB	DB	1 GTGTGTGTGTGTGTGTGTGTGTGT 24
RESULT 38		
AAQ34024	ID	AAQ34024 standard; DNA; 24 BP.
XX	AC	AAQ34024;
XX	DT	25-MAR-2003 (revised)
XX	DT	02-FEB-1993 (first entry)
DE	DE	Microsatellite sequence from clone TGLA423.
XX	PC	PCR; selection; primers; OPTIRIM; breeding; cattle; parentage;
XX	KM	genetic mapping; traits; amplification; ss.
XX	OS	Bos taurus.
XX	PN	MO9213102-A1.
PD	PD	06-AUG-1992.





## RESULT 44

DT 24-APR-2003 (first entry)

DE Human RNA polymerase I-40 kDa subunit 9.68 PCR primer #1.  
 XX  
 XX Human; RNA polymerase I-40 kDa subunit 9.68; cancer; cytostatic;  
 KW HIV infection; anti-HIV; PCR; primer; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 PN CN1363655-A.  
 XX  
 PD 14-AUG-2002.  
 XX  
 PF 05-JAN-2001; 2001CN-00105029.  
 XX  
 PR 05-JAN-2001; 2001CN-00105029.  
 XX  
 PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.  
 XX  
 PI Mao Y, Xie Y;  
 XX  
 DR WPI; 2002-742064/81.  
 XX  
 PT Polypeptide-human RNA polymerase I-40 kDa subunit 9.68 and polynucleotide  
 XX for coding it.  
 PS Example 2; Page 17 (Disclosure); 32pp; Chinese.  
 XX  
 CC The present invention relates to human RNA polymerase I-40 kDa subunit  
 CC 9.68 (see ABP59130). The protein can be used for treating diseases such  
 CC as cancer and HIV infection. The present sequence is a PCR primer, which  
 CC was used in an example from the invention  
 XX  
 SQ Sequence 24 BP; 6 A; 8 C; 5 G; 5 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 1469 GAACCTCTGACCTCAGTGATCA 1492  
 1 GAACCTCTGACCTCAGTGATCA 24  
 XX  
 RESULT 46  
 ACH03377  
 ID ACH03377 standard; DNA; 24 BP.  
 AC ACH03377;  
 XX  
 DT 25-SEP-2003 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #1012.  
 XX  
 KW Immunostimulatory; antiinflammatory; dermatological; antipsoriatic;  
 KW antitumor; gene therapy; vaccine; non-allergic inflammatory disease;  
 KW psoriasis; eczema; allergic contact dermatitis; latex dermatitis;  
 KW inflammatory bowel disease; ulcerative colitis; Crohn's disease; ss.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003050268-A1.  
 XX  
 PD 13-MAR-2003.  
 XX  
 PF 29-MAR-2002; 2002US-00112653.  
 XX  
 PR 29-MAR-2001; 2001US-0279642P.  
 XX  
 PA (KRIE/) KRIEG A M.  
 XX (BERG/) BERG D J.  
 XX  
 PI Krieg AM, Berg DJ;  
 XX  
 DR WPI; 2003-521815/49.

XX  
 XX Treating non-allergic inflammatory diseases, such as psoriasis, eczema,  
 PT allergic contact dermatitis, latex dermatitis or inflammatory bowel  
 PT disease by administering an immunostimulatory nucleic acid.  
 XX  
 PS Disclosure; Page 36; 229pp; English.  
 XX  
 CC The invention describes a method of treating non-allergic inflammatory  
 CC disease comprising administering to a subject having or at risk of  
 CC developing a non-allergic inflammatory disease an immunostimulatory  
 CC nucleic acid for prevention or treatment of the disease. The method is  
 CC useful for treating non-allergic inflammatory diseases, such as  
 CC psoriasis, eczema, allergic contact dermatitis, latex dermatitis or  
 CC inflammatory bowel disease e.g., ulcerative colitis or Crohn's disease.  
 CC This sequence represents an immunostimulatory nucleic acid  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.4%; Score 24; DB 1; Length 24;  
 Best Local Similarity 100.0%; Pred. No. 22;  
 Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 XX  
 DB 4997 TGTGTGTGTGTGTGTGTGTGTGTG 5020  
 1 TGTGTGTGTGTGTGTGTGTGTGTG 24  
 XX  
 RESULT 47  
 ADB37364  
 ID ADB37364 standard; DNA; 24 BP.  
 AC ADB37364;  
 XX  
 DT 04-DEC-2003 (first entry)  
 XX  
 DE Immunostimulatory nucleic acid #978.  
 XX  
 KW ds; allergy; asthma; poly-G nucleic acid; aerosol formulation;  
 KW hypo-responsive subject; immunostimulatory.  
 XX  
 OS Synthetic.  
 XX  
 PN US2003087848-A1.  
 XX  
 PD 08-MAY-2003.  
 XX  
 PF 02-FEB-2001; 2001US-00776479.  
 XX  
 PR 03-FEB-2000; 2000US-0179991P.  
 XX  
 PA (BRAT/) BRATZLER R L.  
 XX (PETE/) PETERSEN D M.  
 XX (FOUR/) FOURON Y.  
 XX  
 PI Bratzler RL, Petersen DM, Fouron Y;  
 XX  
 DR WPI; 2003-657977/62.  
 XX  
 PT Treating and/or preventing allergy or asthma using an immunostimulatory  
 PT nucleic acid alone or in combination with an asthma/allergy medicament.  
 XX  
 PS Disclosure; Page 20; 221pp; English.  
 XX  
 CC The invention relates to a method of treating or preventing allergy or  
 CC asthma which comprises administering to a subject a poly-G nucleic acid  
 CC in an aerosol formulation. The methods and compositions of the present  
 CC invention are useful for diagnosing and/or treating asthma and allergy  
 CC especially in a hypo-responsive subject. The present sequence represents  
 CC an immunostimulatory nucleic acid of the invention.  
 XX  
 SQ Sequence 24 BP; 0 A; 0 C; 12 G; 12 T; 0 U; 0 Other;  
 XX  
 QY Query Match 0.4%; Score 24; DB 1; Length 24;



```

PF 04-APR-1994; 94US-00222177.
XX
XX 21-APR-1989; 89US-00341562.
PR 05-SEP-1991; 91US-00754351.
XX
XX (MARS-) MARSHFIELD CLINIC.
XX
XX Weber JI;
XX
XX WPI; 1997-042299/04.
XX
XX Detection of polymorphic genetic markers of the form (dc-da)n(dc-dt)n -
PT using novel nucleic acid mols. as primers.
XX
XX
XX Example 9; Col 61-62; 186pp; English.
XX
XX The invention relates to the isolation of polymorphic repeat sequences
CC having the sequence (dc-da)n.(dc-dt)n which can be used as genetic
CC markers. Primers based on these sequences can be used to detect these
CC repeats, especially for use in e.g. paternity or maternity testing, human
CC genetic analysis such as linkage analysis of genetic disease, commercial
CC animal or plant breeding or pedigree analysis. The sequences AAT66084-
CC T66107 represent repeat sequences of low informativeness found in
CC specific human genes. This repeat sequence is found in the human
CC chromosomal clone SM13. The sequence is amplified by primers AAT66106-7.
CC (Updated on 25-MAR-2003 to correct PF field.)
XX
SQ Sequence 23 BP; 12 A; 11 C; 0 G; 0 T; 0 U; 0 Other;
XX
Query Match 0.4%; Score 23; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGT 5019
DB 23 TGTGTGTGTGTGTGTGTGTGTGTGT 1
XX
RESULT 52
AAF60472/c
ID AAF60472 standard; DNA; 23 BP.
XX
XX AAF60472;
AC
XX
DT 27-APR-2001 (first entry)
XX
XX Oligonucleotide clamp #17.
DE
XX Oligonucleotide clamp; ds.
KM
XX
XX Unidentified.
CS
XX
XX US6180777-B1.
PN
XX
XX 30-JAN-2001.
PD
XX
XX 03-JAN-1997; 97US-00787321.
PF
XX
XX 12-JAN-1996; 96US-0009918P.
PR
XX
XX (FARB ) BAYER CORP.
PA
XX
XX Horn T;
XX
XX WPI; 2001-201911/20.
DR
XX
XX Synthesizing branched nucleic acids useful as diagnostic and molecular
PT probes, involves combining first units having haloalkylamino groups and
PT second units having thiol or phosphorothioate groups.
XX
XX Example 7; Col 19; 20pp; English.
CC
The present invention relates to a method for synthesising a branched or

```





```

RESULT 55
AAQ3675
ID AAQ3675 standard; DNA; 22 BP.
XX
XX
AC AAQ3675;
XX
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
DE Microsatellite sequence from clone TGLA117.
XX
XX
KM PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KM genetic mapping; traits; amplification; ss.
XX
XX
OS Bos taurus.
XX
XX
PN WO9213102-A1.
XX
XX
PD 06-AUG-1992.
XX
XX
PF 15-JAN-1992; 92WO-US000340.
XX
XX
PR 15-JAN-1991; 91US-00642342.
XX
XX
PA (GENM-) GENMARK.
XX
XX
PI Georges M, Massey JM;
XX
XX
DR WPI; 1992-284684/34.
XX
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX
PS Table 7; Page 199; 517pp; English.
XX
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
XX
XX
Query Match 0.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4997 TGTGTGTGTGTGTGTGTGTGTG 5018
DB 1 TGTGTGTGTGTGTGTGTGTGTG 22

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XX
XX
DE Microsatellite sequence from clone TGLA432.
XX
XX
KM PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KM genetic mapping; traits; amplification; ss.
XX
XX
OS Bos taurus.
XX
XX
PN WO9213102-A1.
XX
XX
PD 06-AUG-1992.
XX
XX
PF 15-JAN-1992; 92WO-US000340.
XX
XX
PR 15-JAN-1991; 91US-00642342.
XX
XX
PA (GENM-) GENMARK.
XX
XX
PI Georges M, Massey JM;
XX
XX
DR WPI; 1992-284684/34.
XX
XX
PT Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX
PS Table 7; Page 346; 517pp; English.
XX
XX
CC The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n > 9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determinism of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
XX
XX
Query Match 0.4%; Score 22; DB 1; Length 22;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4997 TGTGTGTGTGTGTGTGTGTGTG 5018
DB 1 TGTGTGTGTGTGTGTGTGTGTG 22

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RESULT 56
AAQ34038
ID AAQ34038 standard; DNA; 22 BP.
XX
XX
AC AAQ34038;
XX
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)

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RESULT 57
AAQ34080
ID AAQ34080 standard; DNA; 22 BP.
XX
XX
AC AAQ34080;
XX
XX
DT 25-MAR-2003 (revised)
DT 02-FEB-1993 (first entry)
XX
XX
DE Microsatellite sequence from clone TGLA48.
XX
XX
KM PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
KM genetic mapping; traits; amplification; ss.
XX
XX
OS Bos taurus.
XX
XX
PN WO9213102-A1.

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PD 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
PF Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
PR 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
PA
PI Georges M, Massey JM,
XX
XX MPI, 1992-264684/34.
DR
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX Table 7; Page 363; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 22; DB 1; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 29;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4997 TGTGTGTGTGTGTGTGTGTGTG 5018
XX 1 TGTGTGTGTGTGTGTGTGTGTGTG 22
XX
XX RESULT 58
XX AAQ33991
XX ID AAQ33991 standard; DNA, 22 BP.
XX
XX AAQ33991;
XX
XX 25-MAR-2003 (revised)
XX 02-FEB-1993 (first entry)
XX
XX Microsatellite sequence from clone TGLA39.
XX
XX PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage;
XX genetic mapping; traits; amplification; ss.
XX
XX Bos taurus.
XX
XX WO9213102-A1.
XX
XX 06-AUG-1992.
XX
XX 15-JAN-1992; 92WO-US000340.
XX
XX 15-JAN-1991; 91US-00642342.
XX
XX (GENM-) GENMARK.
XX
XX Georges M, Massey JM,
XX
XX

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DR MPI, 1992-264684/34.
XX
XX Polymorphic bovine DNA markers - used in genetic identification, gene
PT mapping, and selective breeding.
XX
XX Table 7; Page 327; 517pp; English.
XX
XX The sequence is that of a bovine microsatellite sequence obtd. by
CC screening a library of bovine MboI DNA fragments of between 250 and 500
CC bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50
CC clones cross-hybridised. Assuming independent distribution of
CC microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites
CC in the bovine genome is estimated at >100, 000. The sequence information
CC for ca. 230 such bovine microsatellites is summarised in the
CC specification and indexed herein (see below). The sequences upstream and
CC downstream of the microsatellite sequence were used to generate the
CC required PCR primers for in vitro amplification of the corresp.
CC microsatellite (using the program OPTIPRIM). The microsatellites may be
CC used to identify individuals, for parentage testing, and in the genetic
CC mapping of economic trait loci, or genes involved the determination of
CC economically important traits esp. in cattle, to allow selective
CC breeding. See also AAQ3501-34437. (Updated on 25-MAR-2003 to correct PN
CC field.)
XX
XX
SQ Sequence 22 BP; 0 A; 0 C; 11 G; 11 T; 0 U; 0 Other;
XX
XX Query Match 0.4%; Score 22; DB 1; Length 22;
XX Best Local Similarity 100.0%; Pred. No. 29;
XX Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX 4997 TGTGTGTGTGTGTGTGTGTGTG 5018
XX 1 TGTGTGTGTGTGTGTGTGTGTGTG 22
XX
XX RESULT 59
XX AAQ83952/C
XX ID AAQ83952 standard; DNA, 22 BP.
XX
XX AAQ83952;
XX
XX 25-MAR-2003 (revised)
XX 04-OCT-1995 (first entry)
XX
XX Oligonucleotide clamp n, for producing comb-type branched polymer.
XX
XX HIV; pol; net; oligonucleotide clamp; branched; macromolecule; ss.
XX
XX Synthetic.
XX
XX Key
XX modified_base 1
XX Location/Qualifiers
XX 1
XX /tag= a
XX /note= "Modified with BrCH2(-O)CNH-"
XX
XX modified_base 8..9
XX /tag= b
XX /note= "C(pnp)A, pnp = a linkage or monomer containing a
XX bromoacetyl amino functionality, and p = phosphodiester
XX linkage"
XX
XX modified_base 14..15
XX /tag= C
XX /note= "C(pnp)A, pnp = a linkage or monomer containing a
XX bromoacetyl amino functionality, and p = phosphodiester
XX linkage"
XX
XX modified_base 21..22
XX /tag= d
XX /note= "C(pnp)A, pnp = a linkage or monomer containing a
XX bromoacetyl amino functionality, and p = phosphodiester
XX linkage"
XX
XX WO9501365-A1.
XX
XX 12-JAN-1995.
XX
XX

```

[illegible]

PI Weber JL;  
DR WPI; 1997-042299/04.  
PT Detection of polymorphic genetic markers of the form (dc-da)n(dc-dt)n -  
XX using novel nucleic acid mols. as primers.  
PS Disclosure; Col 9-10; 186pp; English.

CC The invention relates to the isolation of polymorphic repeat sequences  
CC having the sequence (dc-da)n.(dc-dt)n which can be used as genetic  
CC markers. Primers based on these sequences can be used to detect these  
CC repeats, especially for use in e.g paternity or maternity testing, human  
CC genetic analysis such as linkage analysis of genetic disease, commercial  
CC animal or plant breeding or pedigree analysis. Clones containing the  
CC repeat sequences were isolated by hybridisation of chromosome-specific  
CC phage libraries with a synthetic poly(dc-da).(dc-dt) probe. Over 100  
CC repeat blocks were isolated. The inserts from the clones were amplified  
CC by primers AAT65798-T66047. Those clones where the repeat sequence has  
CC been determined are shown in AAT65704-797. This repeat sequence is from  
CC the marker clone Mdfz5 which contains the repeat sequence having the  
CC formula: (AC)11. (Updated on 25-MAR-2003 to correct PF field.)

SQ Sequence 22 BP; 11 A; 11 C; 0 G; 0 T; 0 U; 0 Other;

Query Match 0.4%; Score 22; DB 1; Length 22;  
Best Local Similarity 100.0%; Pred. No. 29;  
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4996 GGCTGTGCTGTGCTGTGCTGTGCT 5017  
DB 22 GGCTGTGCTGTGCTGTGCTGTGCT 1

RESULT 61.  
AAI64448  
ID AAI64448 standard; DNA; 22 BP.  
XX  
AC AAI64448;  
XX  
DT 23-NOV-2001 (first entry)  
DE SSR motif #8.  
XX  
KW Simple Sequence Repeat; SSR; clover; microsatellite; genome mapping;  
KM trait mapping; marker-assisted selection; gene selection; legume;  
FN DNA profiling; breeding; ds.  
OS Unidentified.  
XX  
NZ509194-A.  
PD 25-MAY-2001.  
XX  
PF 03-JAN-2001; 2001NZ-00509194.  
XX  
PR 24-DEC-1999; 99AU-00004907.  
FR 28-MAR-2000; 2000AU-00006520.  
XX  
PA (AGRI-) AGRIC VICTORIA SERVICES PTY LTD.  
PI Koelliker R, Forster JW;  
XX  
WPI; 2001-431058/46.  
XX  
PT Novel simple sequence repeats in clover species useful for selection of  
PT genes in legume breeding, for profiling legume species varieties and for  
PT testing the purity of legume seed batches.  
PS Claim 6; Page 35; 52pp; English.

CC The present invention relates to Simple Sequence Repeats (SSRs) from  
CC clover species. SSRs, also called microsatellites, are based on a 1-7



ID	AAQ33879		standard; DNA; 21 BP.
XX	AC	AAQ33879;	
XX	DT	25-MAR-2003	(revised)
XX	DT	02-FEB-1993	(first entry)
DE	XX	Microsatellite sequence from clone TGLA301.	
XX	KW	PCR; selection; primers; OPTIRIM; breeding; cattle; parentage;	
XX	KW	genetic mapping; traits; amplification; ss.	
OS	Bos taurus.		
PN	WO9213102-A1.		
PD	06-AUG-1992.		
PX	15-JAN-1992;	92WO-US000340.	
PF	15-JAN-1991;	91US-00642342.	
PR	(GENM-) GENMARK.		
PA	Georges M, Massey JM,		
PI	WPI; 1992-284684/34.		
DR			
XX	Polymorphic bovine DNA markers - used in genetic identification, gene		
PT	mapping, and selective breeding.		
PS	Table 7; Page 281; 517pp; English.		
CC	The sequence is that of a bovine microsatellite sequence obtd. by		
CC	screening a library of bovine MboI DNA fragments of between 250 and 500		
CC	bp with an (AC)15 and a (TC)15 oligonucleotide probe. One out of 50		
CC	clones cross-hybridised. Assuming independent distribution of		
CC	microsatellites and MboI sites, the frequency of (T6)n >9 microsatellites		
CC	in the bovine genome is estimated at >100, 000. The sequence information		
CC	for ca. 230 such bovine microsatellites is summarised in the		
CC	specification and indexed herein (see below). The sequences upstream and		
CC	downstream of the microsatellite sequence were used to generate the		
CC	required PCR primers for in vitro amplification of the corresp.		
CC	microsatellite (using the program OPTIRIM). The microsatellites may be		
CC	used to identify individuals, for parentage testing, and in the genetic		
CC	mapping of economic trait loci, or genes involved in the determination of		
CC	economically important traits esp. in cattle, to allow selective		
CC	breeding. See also AAQ33501-34437. (Updated on 25-MAR-2003 to correct PN		
field.)			
SQ	Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;		
XX			
Query Match	0.3%; Score 21; DB 1; Length 21;		
Best Local Similarity	100.0%; Pred.No. 34;		
Matches 21; Conservative	0; Mismatches	0; Indels	0; Gaps
OY	4597 TGCTGTGCTGTGCTGTGCTGTGCT 5017		
DB	1 TGCTGTGCTGTGCTGTGCTGTGCT 21		
RESULT 65			
ID	AAAX90296		
XX	AAAX90296 standard; DNA; 21 BP.		
XX	AAAX90296;		
XX	24-SEP-1999 (first entry)		
DE	Oligonucleotide RTCo5 used in an Example from US5932556.		
XX	CD28; inhibition; antisense oligonucleotide; interleukin 2; IL-2;		

KW	immune system mediated disease; gamma-interferon; IL-8; ss.	
XX	Synthetic.	
XX	US5932556-A.	
XX		
XX	03-AUG-1999.	
XX		
XX	18-SEP-1995; 95US-00529878.	
XX		
XX	09-FEB-1995; 95US-00387041.	
XX	18-SEP-1995; 95US-00529878.	
XX		
XX	(TAMR/) TAM R C.	
XX		
XX	Tam RC;	
XX		
XX	WPI, 1996-384228/38.	
XX		
XX	Oligo:nucleotide which reduces CD28 gene expression in T cells - for treating immune system diseases, e.g. graft vs. host disease, septic shock, psoriasis, etc.	
XX		
XX	Example; Col 13; 45pp; English.	
XX		
XX	The present invention describes a method for inhibiting the expression of CD28, IL-2, gamma-interferon or IL-8 in a mammal. The method comprises subcutaneous administration of an oligonucleotide (OGN). AAX90288 to AAX90291 represent specifically claimed OGNs for use in the method. The OGNs are used for the treatment of immune system-mediated diseases. AAX90292 to AAX90323 represent oligonucleotides used in the exemplification of the present invention	
XX		
XX	Sequence 21 BP, 0 A, 0 C, 11 G, 10 T, 0 U, 0 Other;	
XX		
XX	Query Match 0.3%; Score 21; DB 1; Length 21;	
XX	Best Local Similarity 100.0%; Pred. No. 34;	
XX	Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
CY	4996 GTGTGTGTGTGTGTGTGTGTGTG 5016	
DB	1 GTGTGTGTGTGTGTGTGTGTGTG 21	
XX		
XX	RESULT 66	
XX	AAT65738/C	
ID	AAT65738 standard; DNA; 21 BP.	
XX		
XX	AAT65738;	
XX		
XX	25-MAR-2003 (revised)	
DT	17-JUN-1997 (first entry)	
XX		
XX	Repeat sequence from polymorphic marker clone Mf37.	
XX		
XX	Polymorphism; repeat sequence; genetic marker; primer; amplification; PCR; polymerase chain reaction; paternity; maternity; human; pedigree; linkage analysis; genetic disease; animal; plant; breeding; locus; hybridisation; chromosome; ds.	
XX		
XX	Homo sapiens.	
OS		
XX	US5582979-A.	
XX		
XX	10-DEC-1996.	
XX		
XX	04-APR-1994; 94US-00222177.	
XX		
XX	21-APR-1989; 89US-00341562.	
XX	05-SEP-1991; 91US-00754351.	
XX		
XX	(MARS-) MARSHFIELD CLINIC.	
XX		



## RESULT 69

AA57495/C

ID AA57495 standard; DNA; 21 BP.

XX AA57495;

DT 20-OCT-2000 (first entry)

XX Primer used for SSCP screening of the human TIGR gene.

XX TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;

XX glaucoma; steroid sensitivity; progressive ocular hypertension;

XX vision loss; primer; ss.

XX Homo sapiens.

XX WO200042220-A1.

XX 20-JUL-2000.

XX 11-JAN-2000; 2000WO-US000559.

XX 11-JAN-1999; 99US-00227881.

XX 07-MAY-1999; 99US-00306828.

XX (REGC ) UNIV CALIFORNIA.

XX Nguyen TD, Polansky JR, Chen P, Chen H;

XX WPI; 2000-491060/43.

XX diagnosis, prognosis and treatment of glaucoma, based on detecting

XX specific polymorphisms in the promoter of the trabecular meshwork

XX inducible glucocorticoid receptor gene.

XX Claim 9; Page 53; 122pp; English.

XX Primers AA57489-A57508 were used for single strand conformational  
 CC polymorphism (SSCP) screening of the human TIGR (trabecular meshwork  
 CC inducible glucocorticoid receptor) gene. The primers correspond to  
 CC sequences found within the TIGR promoter and two of the exons of TIGR,  
 CC and are used in the method of the invention. The specification describes  
 CC a method for the diagnosis, prognosis and treatment of glaucoma, based on  
 CC detecting specific polymorphisms in the promoter of the TIGR gene. The  
 CC method is used for diagnosis and prognosis of glaucoma (of all types),  
 CC steroid sensitivity and progressive ocular hypertension that leads to  
 CC loss of vision. Glaucoma can be treated by administering an agent that  
 CC binds to cis-acting elements within the TIGR promoter. The TIGR promoter  
 CC (or other regulatory regions) can be used to express homologous or  
 CC heterologous genes, particularly for tissue-specific expression of  
 CC therapeutic transgenes for treating glaucoma, also to generate transgenic  
 CC animals and in screening for compounds (specific modulators) with  
 CC diagnostic or therapeutic potential. Fragments of the TIGR sequence can  
 CC be used as amplification primers or probes, e.g. for isolating related  
 CC sequences in non-human animals

SQ Sequence 21 BP; 8 A; 6 C; 3 G; 4 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4394 CAGTTGTCAGATACCTTGT 4414

DB 21 CAGTTGTCAGATACCTTGT 1

## RESULT 70

AA57491/C

ID AA57491 standard; DNA; 21 BP.

XX AA57491;

XX AC

XX XX

DT 20-OCT-2000 (first entry)

XX Primer used for SSCP screening of the human TIGR gene.

XX TIGR; trabecular meshwork inducible glucocorticoid receptor; promoter;

XX glaucoma; steroid sensitivity; progressive ocular hypertension;

XX vision loss; primer; ss.

XX Homo sapiens.

XX WO200042220-A1.

XX 20-JUL-2000.

XX 11-JAN-2000; 2000WO-US000559.

XX 11-JAN-1999; 99US-00227881.

XX 07-MAY-1999; 99US-00306828.

XX (REGC ) UNIV CALIFORNIA.

XX Nguyen TD, Polansky JR, Chen P, Chen H;

XX WPI; 2000-491060/43.

XX diagnosis, prognosis and treatment of glaucoma, based on detecting

XX specific polymorphisms in the promoter of the trabecular meshwork

XX inducible glucocorticoid receptor gene.

XX Claim 9; Page 53; 122pp; English.

XX Primers AA57489-A57508 were used for single strand conformational  
 CC polymorphism (SSCP) screening of the human TIGR (trabecular meshwork  
 CC inducible glucocorticoid receptor) gene. The primers correspond to  
 CC sequences found within the TIGR promoter and two of the exons of TIGR,  
 CC and are used in the method of the invention. The specification describes  
 CC a method for the diagnosis, prognosis and treatment of glaucoma, based on  
 CC detecting specific polymorphisms in the promoter of the TIGR gene. The  
 CC method is used for diagnosis and prognosis of glaucoma (of all types),  
 CC steroid sensitivity and progressive ocular hypertension that leads to  
 CC loss of vision. Glaucoma can be treated by administering an agent that  
 CC binds to cis-acting elements within the TIGR promoter. The TIGR promoter  
 CC (or other regulatory regions) can be used to express homologous or  
 CC heterologous genes, particularly for tissue-specific expression of  
 CC therapeutic transgenes for treating glaucoma, also to generate transgenic  
 CC animals and in screening for compounds (specific modulators) with  
 CC diagnostic or therapeutic potential. Fragments of the TIGR sequence can  
 CC be used as amplification primers or probes, e.g. for isolating related  
 CC sequences in non-human animals

SQ Sequence 21 BP; 8 A; 8 C; 2 G; 3 T; 0 U; 0 Other;

Query Match 0.3%; Score 21; DB 1; Length 21;

Best Local Similarity 100.0%; Pred. No. 34;

Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5047 CTATTATGGGATGGGATGTC 5067

DB 21 CTATTATGGGATGGGATGTC 1

## RESULT 71

AAH46013

ID AAH46013 standard; DNA; 21 BP.

XX AAH46013;

XX 12-SEP-2001 (first entry)

XX Synthetic oligonucleotide 13.

XX Synthetic oligonucleotide repeat; cytosinatic; apoptosis;

XX cell cycle arrest; cell proliferation; caspase; cytokine; interleukin;





XX (IOWA ) UNIV IOWA RES FOUND.  
 PA (COLE-) COLEY PHARM GMBH.  
 XX Krieg AM, Schetter C, Vollmer U;  
 PI WPI; 2001-273485/28.  
 DR  
 XX  
 PT Vaccinating against tumors, infectious diseases, allergies and asthma  
 PT using immunostimulatory Py-rich and TG nucleic acids.  
 XX  
 PS Claim 101, Page 56, 338pp, English.  
 XX  
 CC The present invention relates to a method for stimulating an immune  
 CC response. The method comprises administering an immunostimulatory nucleic  
 CC acid to a non-tumor subject in sufficient quantity to stimulate an  
 CC immune response. The present sequence is one such immunostimulatory  
 CC nucleic acid. The immunostimulatory nucleic acids can be pyrimidine rich  
 CC (py-rich) or thymidine (T) rich. The method is used to vaccinate subjects  
 CC against tumour antigens, viral antigens (e.g. herpesviridae, retroviridae  
 CC and/or orthomyxoviridae), bacterial antigens (e.g. toxoplasma,  
 CC haemophilus, campylobacter, clostridium, Escherichia coli and/or  
 CC staphylococcus), fungal antigens and/or parasitic antigens. The method is  
 CC also useful for preventing cancer, asthma, infectious disease, allergy or  
 CC immune deficiency. The present sequence can also be used to redirect a  
 CC Th2 to a Th1 immune response and to activate immune cells. Note: the  
 CC present sequence may have a phosphorothioate backbone.  
 CC  
 SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4997 TGTGTGTGTGTGTGTGTGTGT 5017  
 Db 1 TGTGTGTGTGTGTGTGTGTGT 21  
 RESULT 74  
 ABS78423  
 ID ABS78423 standard; DNA; 21 BP.  
 XX  
 AC ABS78423;  
 XX  
 DT 13-DEC-2002 (first entry)  
 XX  
 DE Angiogenesis inhibitory oligonucleotide #907.  
 XX  
 KM Angiogenesis inhibitor; ss; angiogenesis; solid tumour growth;  
 KM tumour metastasis; precancerous lesion; rheumatoid arthritis; psoriasis;  
 KM diabetic retinopathy; retinopathy of prematurity; macular degeneration;  
 KM corneal graft rejection; neovascular glaucoma; retrolental fibroplasia;  
 KM rubecosis; Osler-Webber Syndrome; myocardial angiogenesis;  
 KM plaque neovascularisation; telangiectasia; haemophilic joint;  
 KM angiodibroma; wound granulation; intestinal adhesion; atherosclerosis;  
 KM scleroderma; hypertrophic scar.  
 XX  
 OS Synthetic.  
 OS  
 PN WO200253141-A2.  
 XX  
 PD 11-JULY-2002.  
 XX  
 PF 14-DEC-2001; 2001WO-US048458.  
 XX  
 PR 14-DEC-2000; 2000US-0255534P.  
 XX  
 PA (COLE-) COLEY PHARM GROUP INC.  
 XX  
 PI Bratzler RL;  
 XX  
 DR WPI; 2002-566690/60.

XX Inhibiting angiogenesis in a subject, involves administering at least one  
 PT antiangiogenic nucleic acid molecule to the subject.  
 XX  
 PS Claim 2, Page 35; 276pp; English.  
 XX  
 CC The invention relates to inhibiting angiogenesis in a subject, comprising  
 CC administering at least one antiangiogenic nucleic acid molecule. Also  
 CC included is a kit comprising a first container housing the antiangiogenic  
 CC nucleic acids, and instructions for administering them to a subject  
 CC having a condition characterised by unwanted angiogenesis. The method is  
 CC useful for inhibiting angiogenesis associated with solid tumour growth,  
 CC tumour metastasis, precancerous lesion, rheumatoid arthritis, psoriasis,  
 CC diabetic retinopathy, retinopathy of prematurity, macular degeneration,  
 CC corneal graft rejection, neovascular glaucoma, retrolental fibroplasia,  
 CC rubecosis, Osler-Webber Syndrome, myocardial angiogenesis, plaque  
 CC neovascularisation, telangiectasia, haemophilic joints, angiodibroma,  
 CC wound granulation, intestinal adhesions, atherosclerosis, scleroderma and  
 CC hypertrophic scars. The present sequence is an antiangiogenic nucleic  
 CC acid of the invention  
 CC  
 SQ Sequence 21 BP; 0 A; 0 C; 10 G; 11 T; 0 U; 0 Other;  
 Query Match 0.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 34;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 4997 TGTGTGTGTGTGTGTGTGTGT 5017  
 Db 1 TGTGTGTGTGTGTGTGTGTGT 21  
 RESULT 75  
 ACF64053  
 ID ACF64053 standard; DNA; 21 BP.  
 XX  
 AC ACF64053;  
 XX  
 DT 13-OCT-2003 (first entry)  
 XX  
 DE IFNARI forward PCR primer #29.  
 XX  
 KM Human; detection; computer-readable storage medium; polymorphic site;  
 KM signal carrying data; data processing system; multiple sclerosis;  
 KM PCR primer; ss.  
 XX  
 OS Homo sapiens.  
 OS  
 OS Synthetic.  
 PN WO2003014319-A2.  
 XX  
 PD 20-FEB-2003.  
 XX  
 PF 07-AUG-2002; 2002WO-US05268.  
 XX  
 PR 07-AUG-2001; 2001US-0310741P.  
 PR 24-SEP-2001; 2001US-0324790P.  
 XX  
 PA (DNAS-) DNA SCI INC.  
 XX  
 PI Jones HB, Xu H, White R, Rienhoff HY, Jin W, Natsoulis G;  
 PT WPI; 2003-268196/26.  
 XX  
 PT New polynucleotide, useful for detecting loci associated with multiple  
 PT sclerosis.  
 XX  
 PS Disclosure, Page 10, 93pp, English.  
 XX  
 CC The present invention describes an isolated polynucleotide (PN)  
 CC comprising: (a) a sequence comprising at least 15 contiguous nucleotides  
 CC of a sequence comprising variant sequences (A) from Table 4 given in the  
 CC specification; or (b) a sequence that is complementary to (A). Also



GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 09:57:08 / Search time 6 seconds  
(without alignments)  
3.656 Million cell updates/sec

Title: US-09-227-881-3  
Perfect score: 6169  
Sequence: 1 atcttgcagttactctc.....ctgtgcctccatcagcag 6169

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapext 0.5

Searched: 77 seqs, 1778 residues

Total number of hits satisfying chosen parameters: 154

Minimum DB seq length: 12  
Maximum DB seq length: 250

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 78 summaries

Database: rn13.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	227	3.7	227 1	US-09-306-828-38
2	29	0.5	29 1	US-08-822-999-8
3	29	0.5	29 1	US-09-056-285A-11
4	28	0.5	28 1	US-08-222-177A-451
5	27	0.4	27 1	US-08-455-627-23
6	27	0.4	27 1	US-08-222-177A-143
7	27	0.4	27 1	US-08-689-856-23
8	25	0.4	25 1	US-08-222-177A-146
9	25	0.4	25 1	US-08-222-177A-145
10	24	0.4	24 1	US-08-222-177A-445
11	23	0.4	23 1	US-08-222-177A-454
12	23	0.4	23 1	US-08-787-321-22
13	22.4	0.4	227 1	US-09-306-828-38
14	22	0.4	22 1	US-08-222-177A-125
15	21	0.3	21 1	US-08-529-878B-9
16	21	0.3	21 1	US-08-938-669A-8
17	21	0.3	21 1	US-08-938-669A-12
18	21	0.3	21 1	US-08-938-669A-13
19	21	0.3	21 1	US-09-306-828-12
20	21	0.3	21 1	US-09-306-828-18
21	20	0.3	20 1	US-08-863-639A-32
22	20	0.3	20 1	US-09-407-675-5
23	20	0.3	20 1	US-08-938-669A-7
24	20	0.3	20 1	US-08-938-669A-9
25	20	0.3	20 1	US-08-938-669A-10
26	20	0.3	20 1	US-08-938-669A-13
27	20	0.3	20 1	US-08-938-669A-19
28	20	0.3	20 1	US-09-488-671-88
29	20	0.3	20 1	US-09-467-642-73
30	20	0.3	20 1	US-09-180-903-8
31	20	0.3	20 1	US-09-056-285A-16
32	20	0.3	20 1	US-09-056-285A-20
33	20	0.3	20 1	US-09-056-285A-21

34	20	0.3	20 1	US-09-056-285A-22	Sequence 22, Appl
35	20	0.3	20 1	US-09-056-285A-23	Sequence 23, Appl
36	20	0.3	20 1	US-09-056-285A-25	Sequence 25, Appl
37	20	0.3	20 1	US-09-056-285A-26	Sequence 26, Appl
38	20	0.3	20 1	US-09-056-285A-27	Sequence 27, Appl
39	20	0.3	20 1	US-09-780-115-25	Sequence 28, Appl
40	20	0.3	20 1	US-09-607-529-3	Sequence 29, Appl
41	20	0.3	20 1	US-09-306-828-7	Sequence 30, Appl
42	20	0.3	20 1	US-09-306-828-9	Sequence 31, Appl
43	20	0.3	20 1	US-09-306-828-10	Sequence 32, Appl
44	20	0.3	20 1	US-09-306-828-13	Sequence 33, Appl
45	20	0.3	20 1	US-09-306-828-19	Sequence 34, Appl
46	20	0.3	20 1	US-09-060-259-457	Sequence 35, Appl
47	20	0.3	20 1	US-09-402-923A-257	Sequence 36, Appl
48	19	0.3	19 1	US-08-222-177A-442	Sequence 37, Appl
49	19	0.3	19 1	US-08-629-939-10	Sequence 38, Appl
50	19	0.3	19 1	US-08-759-873-10	Sequence 39, Appl
51	19	0.3	19 1	US-08-915-609-3	Sequence 40, Appl
52	19	0.3	19 1	US-08-915-609-4	Sequence 41, Appl
53	19	0.3	19 1	US-08-938-669A-11	Sequence 42, Appl
54	19	0.3	19 1	US-08-938-669A-14	Sequence 43, Appl
55	19	0.3	19 1	US-08-938-669A-15	Sequence 44, Appl
56	19	0.3	19 1	US-08-938-669A-17	Sequence 45, Appl
57	19	0.3	19 1	US-08-938-669A-22	Sequence 46, Appl
58	19	0.3	19 1	US-08-938-669A-24	Sequence 47, Appl
59	19	0.3	19 1	US-09-056-285A-19	Sequence 48, Appl
60	19	0.3	19 1	US-09-306-828-11	Sequence 49, Appl
61	19	0.3	19 1	US-09-306-828-14	Sequence 50, Appl
62	19	0.3	19 1	US-09-306-828-15	Sequence 51, Appl
63	19	0.3	19 1	US-09-306-828-17	Sequence 52, Appl
64	19	0.3	19 1	US-09-306-828-22	Sequence 53, Appl
65	19	0.3	19 1	US-09-306-828-24	Sequence 54, Appl
66	19	0.3	19 1	US-09-306-828-35	Sequence 55, Appl
67	19	0.3	19 1	US-09-306-828-36	Sequence 56, Appl
68	18	0.3	18 1	US-08-700-530-1	Sequence 57, Appl
69	18	0.3	18 1	US-08-700-530-2	Sequence 58, Appl
70	18	0.3	18 1	US-08-976-427-28	Sequence 59, Appl
71	18	0.3	18 1	US-09-648-312-28	Sequence 60, Appl
72	18	0.3	18 1	US-09-056-285A-17	Sequence 61, Appl
73	18	0.3	18 1	US-09-056-285A-18	Sequence 62, Appl
74	18	0.3	18 1	US-09-056-285A-24	Sequence 63, Appl
75	17	0.3	17 1	US-08-222-177A-448	Sequence 64, Appl
76	17	0.3	17 1	US-08-885-126-9	Sequence 65, Appl
77	17	0.3	17 1	US-08-966-111-11	Sequence 66, Appl
78	17	0.3	17 1	US-09-490-774-11	Sequence 67, Appl

ALIGNMENTS

RESULT 1  
US-09-306-828-38  
Sequence 38, Application US/09306828  
Patent No. 6475724  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
APPLICANT: Chen, Pu  
APPLICANT: Chen, Hua  
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis  
CURRENT APPLICATION NUMBER: US/09/306,828  
CURRENT FILING DATE: 1999-05-07  
EARLIER APPLICATION NUMBER: US 09/227,881  
EARLIER FILING DATE: 1999-01-11  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 38  
LENGTH: 227  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-828-38  
Query Match 3.7%, Score 227, DB 1, Length 227;

Best Local Similarity 100.0%; Pred. No. 1.4e-19;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5045 AACATATATGGGGATGAGTGCATTAATTTGGAGTCTTTTAAAGAACTCCAAA 5104

Db 1 AACTATATATGGGGATGAGTGCATTAATTTGGAGTCTTTTAAAGAACTCCAAA 60

QY 5105 CAGACTTCTGGAAGTTATTTCTTAAGAAATCTCTGGACCGGAAAGCAACCCCTG 5164

Db 61 CAGACTTCTGGAAGTTATTTCTTAAGAAATCTCTGGACCGGAAAGCAACCCCTG 120

QY 5165 TGCAAGCCGCCAGCCGCTCAGCGGCACTCTGTTTCCCAATGAAGAGGCTGCTC 5224

Db 121 TGCAAGCCGCCAGCCGCTCAGCGGCACTCTGTTTCCCAATGAAGAGGCTGCTC 180

QY 5225 CCCAGTATATATAACCTCTCTGAGCTCGGAGCTGAGCCAGCAAG 5271

Db 181 CCCAGTATATATAACCTCTCTGAGCTCGGAGCTGAGCCAGCAAG 227

## RESULT 2

US-08-822-999-8  
; Sequence 8, Application US/08822999

; Patent No. 6271026

; GENERAL INFORMATION:

; APPLICANT: Stone, Edwin M.

; APPLICANT: Sheffield, Val C.

; APPLICANT: Alward, Wallace L.M.

; TITLE OF INVENTION: GLAUCOMA COMPOSITIONS AND THERAPEUTIC

; TITLE OF INVENTION: AND DIAGNOSTIC USES THEREFOR

; NUMBER OF SEQUENCES: 18

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/822,999

; FILING DATE: 21-MAR-1997

; CLASSIFICATION: 514

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/791,347

; FILING DATE: 30-JAN-1997

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/748,479

; FILING DATE: 08-NOV-1996

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/234,218

; FILING DATE: 28-APR-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Arnold, Beth E.

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: UIA-010.27

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 8:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 29 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA

; US-08-822-999-8

; Query Match

0.5%; Score 29; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 5.2;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGCTGCAGAGGAGCTGGGACCCCTG 5708

Db 1 AGGGCTGCAGAGGAGCTGGGACCCCTG 29

## RESULT 3

US-03-056-285A-11  
; Sequence 11, Application US/09056285A

; Patent No. 6403307

; GENERAL INFORMATION:

; APPLICANT: Stone, Edwin M.

; APPLICANT: Sheffield, Val C.

; APPLICANT: Alward, Wallace L.M.

; TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS

; NUMBER OF SEQUENCES: 43

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY, HOAG & ELIOT LLP

; STREET: One Post Office Square

; CITY: Boston

; STATE: MA

; COUNTRY: USA

; ZIP: 02109-2170

; COMPUTER READABLE FORM:

; MEDIUM TYPE: floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentin Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/056,285A

; FILING DATE: 07-Apr-1998

; ATTORNEY/AGENT INFORMATION:

; NAME: Arnold, Beth E.

; REGISTRATION NUMBER: 35,430

; REFERENCE/DOCKET NUMBER: UIA-010.28

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 617-832-1000

; TELEFAX: 617-832-7000

; INFORMATION FOR SEQ ID NO: 11:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 28 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; SEQUENCE DESCRIPTION: SEQ ID NO: 11:

US-03-056-285A-11

; Query Match

0.5%; Score 29; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 5.2;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGCTGCAGAGGAGCTGGGACCCCTG 5708

Db 1 AGGGCTGCAGAGGAGCTGGGACCCCTG 29

## RESULT 4

US-08-222-177A-451/C  
; Sequence 451, Application US/08222177A

; Patent No. 5582979

; GENERAL INFORMATION:

; APPLICANT: Weber, James L.

; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN

; TITLE OF INVENTION: (dc-da)n, (dg-dt)n SEQUENCES AND METHODS OF USING SAME

; NUMBER OF SEQUENCES: 460

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Demilt Ross & Stevens, S.C.

; STREET: 8000 Excelsior Drive, Suite 401

; CITY: Madison

; US-08-222-177A-451/C

; Query Match

0.5%; Score 29; DB 1; Length 29;

Best Local Similarity 100.0%; Pred. No. 5.2;

Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGCTGCAGAGGAGCTGGGACCCCTG 5708

Db 1 AGGGCTGCAGAGGAGCTGGGACCCCTG 29

```

      / INFORMATION FOR SEQ ID NO: 23:
      / SEQUENCE CHARACTERISTICS:
      / LENGTH: 27 nucleotides
      / TYPE: nucleic acid
      / STRANDEDNESS: single
      / TOPOLOGY: linear
      / MOLECULE TYPE: DNA
      / US-08-455-627-23
    Qy Query Match          0.4%; Score 27; DB 1; Length 27;
       Best Local Similarity 100.0%; Pred.No.7.4; Gaps 0;
       Matches 27; Conservative 0; Mismatches 0; Indels 0;
                                     4996 GTGTGTTGTTGTGTGTGTGTG 5022
                                         |||||
Db     27 GTGTGTTGTTGTGTGTGTGTGTGTG 1

RESULT 6
US-08-222-177A-143/c
; Sequence 143, Application US/08222177A
; Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
TITILE OF INVENTION: (dC-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 460
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dewitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CITY: Madison
STATE: Wisconsin
CCOUNTRY: USA
ZIP: 53717-1914
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/222.177A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 07/341,562
FILING DATE: 21-APR-1989
ATTORNEY/AGENT INFORMATION:
NAME: Sara, Charles S.
REGISTRATION NUMBER: 30,492
REFERENCE/DOCKET NUMBER: 09865.601
TELECOMMUNICATION INFORMATION:
TELEPHONE: (608) 831-2100
TELEFAX: (608) 831-2106
TELEX:
INFORMATION FOR SEQ ID NO: 143:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomicc)
IMMEDIATE SOURCE:
CLONE: mfd3lrs
/ 
/ 
US-08-222-177A-143
Qy Query Match          0.4%; Score 27; DB 1; Length 27;
       Best Local Similarity 100.0%; Pred.No.7.4; Gaps 0;
       Matches 27; Conservative 0; Mismatches 0; Indels 0;
                                     4997 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5023
                                         |||||
Db     27 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

```

```

RESULT 7
US-08-689-856-23/c
Sequence 23, Application US/08899856
Patent No. 5830658
GENERAL INFORMATION:
APPLICANT: Sergei M. Gryaznov
TITLE OF INVENTION: Convergent Synthesis of Branched and Multiply
TITLE OF INVENTION: Connected Macromolecular Structures
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooley Godward LLP
STREET: Five Palo Alto Square, 3000 El Camino Real
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94306-2155
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/889,856
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/455,627
FILING DATE: 31-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Jackie N.
REGISTRATION NUMBER: 35,966
REFERENCE/DOCKET NUMBER: LYNX-003/01 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-843-5000
TELEFAX: 415-857-0653
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 27 nucleotides
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-689-856-23

Query Match          0.4%; Score 27; DB 1; Length 27;
Best Local Similarity 100.0%; Pred. No. 7.4;
Matches    27; Conservative   0; Mismatches     0; Indels    0; Gaps      0.

OY      4996 GTGTGTTGTGTGTGTGTGTGTGTGTGTGTG 5022
           |||||
Db       27 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGTG 1

RESULT 8
US-08-787-321-23/c
Sequence 23, Application US/08787321A
Patent No. 6180777
GENERAL INFORMATION:
APPLICANT: Horn, Thomas
TITLE OF INVENTION: SYNTHESIS OF BRANCHED NUCLEIC ACIDS
FILE REFERENCE: (11300)-1199.002
CURRENT APPLICATION NUMBER: US/08/787,321A
CURRENT FILING DATE: 1997-01-03
EARLIER APPLICATION NUMBER: US PROV 60/009,918
EARLIER FILING DATE: 1996-01-12
NUMBER OF SEQ ID NOS: 27
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 23
LENGTH: 27
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
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[illegible]

schultz881-3.rni

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[illegible]







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RESULT 19
US-09-306-828-8/c
; Sequence 8, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-8

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
5047 CTATTATTGGGGTATGGGTGC 5067
DB
21 CTATTATTGGGGTATGGGTGC 1

RESULT 20
US-09-306-828-12/c
; Sequence 12, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 12
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-12

Query Match
Best Local Similarity 100.0%; Score 21; DB 1; Length 21;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
4394 CAGTGTGGCGATACGTTGT 4414
DB
21 CAGTGTGGCGATACGTTGT 1

RESULT 21
US-08-863-639A-32/c
; Sequence 32, Application US/08863639A
; Patent No. 5981185
; GENERAL INFORMATION:
; APPLICANT: Watson, Robert S.
; APPLICANT: Cassin, Peter J.
; APPLICANT: Rampal, Jang B.
; APPLICANT: Caskey, C. T.
```

```
; TITLE OF INVENTION: OLIGONUCLEOTIDE REPEAT ARRAYS
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheldon & Wak
; STREET: 225 South Lake Avenue, 9th Floor
; CITY: Pasadena
; STATE: CA
; COUNTRY: USA
; ZIP: 91101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 3.50 inch, 1.44 Mb storage
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Corel WordPerfect 8 version
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/863,639A
; FILING DATE: May 28, 1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Joseph E. Mueeth
; REGISTRATION NUMBER: 20,532
; REFERENCE/DOCKET NUMBER: 11859-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (626) 796-4000
; TELEFAX: (626) 795-6321
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: Other nucleic acid
US-08-863-639A-32

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY
4996 GTGTGTGTGTGTGTGTGTGT 5015
DB
20 GTGTGTGTGTGTGTGTGTGT 1

RESULT 22
US-09-407-675-5/c
; Sequence 5, Application US/09407675
; Patent No. 6169176
; GENERAL INFORMATION:
; APPLICANT: Bruice, Thomas C.
; APPLICANT: Arya, Dev P.
; TITLE OF INVENTION: DEOXYNUCLEIC ALKYL THIUREA COMPOUNDS AND USES THEREOF
; FILE REFERENCE: 30448.65US02
; CURRENT APPLICATION NUMBER: US/09/407,675
; CURRENT FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: 09/347,443
; PRIOR FILING DATE: 1999-07-02
; PRIOR APPLICATION NUMBER: 60/091,481
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: 60/111,800
; PRIOR FILING DATE: 1998-12-11
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 20
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Oligo 5
US-09-407-675-5

Query Match
Best Local Similarity 100.0%; Score 20; DB 1; Length 20;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```



ATTORNEY/AGENT INFORMATION:  
NAME: Mendelson, Elliot  
REGISTRATION NUMBER: P-42,878  
REFERENCE/DOCKET NUMBER: 07425-0034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 383-6857  
TELEFAX: 202 383-6610  
TELEX:  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-938-669A-10

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4581 CTGAGAGAGTTCCTCCAGAT 4600  
DB 20 CTGAGAGAGTTCCTCCAGAT 1

RESULT 26  
US-08-938-669A-13  
Sequence 13, Application US/08938669A  
Patent No. 6171788  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
TITLE OF INVENTION: RELATED DISEASES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,669A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/791,154  
FILING DATE: 28-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mendelson, Elliot  
REGISTRATION NUMBER: P-42,878  
REFERENCE/DOCKET NUMBER: 07425-0034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 383-6857  
TELEFAX: 202 383-6610  
TELEX:  
INFORMATION FOR SEQ ID NO: 13:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-938-669A-13

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3933 TCAGCTTACTGACAGACC 3952  
DB 1 TCAGCTTACTGACAGACC 20

RESULT 27  
US-08-938-669A-19  
Sequence 19, Application US/08938669A  
Patent No. 6171788  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
TITLE OF INVENTION: RELATED DISEASES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,669A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/791,154  
FILING DATE: 28-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mendelson, Elliot  
REGISTRATION NUMBER: P-42,878  
REFERENCE/DOCKET NUMBER: 07425-0034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 383-6857  
TELEFAX: 202 383-6610  
TELEX:  
INFORMATION FOR SEQ ID NO: 19:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-938-669A-19

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5643 ACCTTGACCGAGCTCCGAG 5662  
DB 1 ACCTTGACCGAGCTCCGAG 20

RESULT 28  
US-08-488-671-88/C  
Sequence 88, Application US/09488671A  
Patent No. 6187545  
GENERAL INFORMATION:  
APPLICANT: Robert McKay  
APPLICANT: Madeline M. Butler  
APPLICANT: Jacqueline Wyatt  
APPLICANT: Lex M. Cossett  
TITLE OF INVENTION: ANTISENSE MODULATION OF PEPCK-CYTOSOLIC EXPRESSION  
FILE REFERENCE: RTS-0123

schul tz881-3.rn1

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:
: CURRENT APPLICATION NUMBER: US/09/488,671A
: CURRENT FILING DATE: 2009-01-21
: NUMBER OF SEQ ID NOS: 177
: SEQ ID NO 88
: LENGTH: 20
: TYPE: DNA
: ORGANISM: Artificial Sequence
: FEATURES:
: OTHER INFORMATION: Antisense Oligonucleotide
US-09-488-671-88

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Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 24;		
Matches 20;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0

QY	4996	GTGTGTGTGTGTGTGT	5013
Db	20	GTGTGTGTGTGTGTGT	1

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RESULT 29
US-09-467-642-73/c
Sequence 73, Application US/09467642
Patent No. 6300132
GENERAL INFORMATION:
APPLICANT: Brett P. Monia
TITLE OF INVENTION: ANTISENSE MODULATION OF TELOMERIC REPEAT BINDING FACTOR 2 EXPRESSION
FILE REFERENCE: PRS-0106
CURRENT APPLICATION NUMBER: US/09/467,642
CURRENT FILING DATE: 1999-12-20
NUMBER OF SEQ ID NOS: 89
SEQ ID NO 73
LENGTH: 20
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Antisense Oligonucleotide
US-09-467-642-73

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Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 24;		
Matches 20; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0

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QY      1513 TGCTGGGATTACAGGCATGA 1532
          |||||
Db      20  TGCTGGGATTACAGGCATGA 1

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RESULT 30  
US-09-180-903-8  
; Sequence 8, Application US/09180903

GENERAL INFORMATION:  
APPLICANT: Rein, Alan

Henderson, Louis E.  
TITLE OF INVENTION: Oligonucleotides Which Specifically Bind  
Retroviral Nucleocapsid Proteins

NUMBER OF SEQUENCES: 15  
CORRESPONDENCE ADDRESS: 1

ADDRESS: 10140 Avenida Las Comarcas, Suite 200  
STREET: Two Embarcadero Center, Eighth Floor  
CITY: San Francisco  
STATE: California

COUNTRY: USA  
ZIP: 94111-3834

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; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDITEM TYPE: EJC001

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;
; MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS

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SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,903
FILING DATE: 12-Jul-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/017,128
FILING DATE: 20-MAY-1996
APPLICATION NUMBER: WO PCT/US97/08936
FILING DATE: 19-MAY-1997
ATTORNEY/AGENT INFORMATION:
NAME: Choi, Kathleen L.
REGISTRATION NUMBER: 43,433
REFERENCE/DOCKET NUMBER: 015280-279100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
SEQUENCE DESCRIPTION: SEQ ID NO: 8:
US-09-180-903-8

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Query Match	0.3%;	Score 20;	DB 1;	Length 20;
Best Local Similarity	100.0%;	Pred. No. 24;		
Matches	20;	Conservative	0;	Mismatches 0;
				Indels 0;
				Gaps 0;

QY	4997	TGTGTGTGTGTGTGTGTG	5016
Db	1	TGTGTGTGTGTGTGTG	20

RESULT 31  
US-09-056-285A-16  
; Sequence 16, Application US/09056285A

GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.

Alward, Wallace L.M  
Fingert, John

NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: POLY HOAG &

STREET: One Post Office S  
CITY: Boston  
STATE: MA

COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:

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; MEDIUM LIFE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/
;

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SOFTWARE: FACSIMILE RELEASE  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09

ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.

REFERENCE/DOCKET NUMBER:  
TELECOMMUNICATION INFORMATION:

TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 16:

SEQUENCE (Nucleotide):  
LENGTH: 20 base pairs  
TYPE: nucleic acid

STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 16:  
US-09-056-285A-16

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5216 GGCTGGCTCCCGAGTATATA 5235  
DB 1 GGCTGGCTCCCGAGTATATA 20

RESULT 32  
US-09-056-285A-20  
Sequence 20, Application US/09056285A  
Patent No. 6403307

GENERAL INFORMATION:

APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.M.  
Fingert, John

TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,285A

FILING DATE: 07-Apr-1998

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: UIA-010.28

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 20:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 20:

US-09-056-285A-20

Query Match 0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 24;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5466 AGTGGCCGATGCCAGTATAC 5485

DB 1 AGTGGCCGATGCCAGTATAC 20

RESULT 33

US-09-056-285A-21/c

Sequence 21, Application US/09056285A

Patent No. 6403307

GENERAL INFORMATION:

APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.M.  
Fingert, John

TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/056,285A

FILING DATE: 07-Apr-1998

ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.

REGISTRATION NUMBER: 35,430

REFERENCE/DOCKET NUMBER: UIA-010.28

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000

TELEFAX: 617-832-7000

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: other nucleic acid

DESCRIPTION: /desc = "primer"

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-056-285A-21

Query Match 0.3%; Score 20; DB 1; Length 20;

Best Local Similarity 100.0%; Pred. No. 24; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5635 ACCAATTGACCTTGACGACG 5654

DB 20 ACCAATTGACCTTGACGACG 1

RESULT 34

US-09-056-285A-22

Sequence 22, Application US/09056285A

Patent No. 6403307

GENERAL INFORMATION:

APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.M.  
Fingert, John

TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY, HOAG & ELIOT LLP

STREET: One Post Office Square

CITY: Boston

STATE: MA

COUNTRY: USA

ZIP: 02109-2170

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

Thu Sep 23 10:01:07 2004

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Page 13

APPLICATION NUMBER: US/09/056,285A  
FILING DATE: 07-Apr-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-010.28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 22:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 22:  
US-09-056-285A-22

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5533 AGCCCATGTCAGTCATCCAT 5552  
DB 1 AGCCCATGTCAGTCATCCAT 20

RESULT 35  
US-09-056-285A-23/c  
Sequence 23, Application US/09056285A  
Patent No. 6403307  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.M.  
Fingert, John  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,285A  
FILING DATE: 07-Apr-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-010.28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 23:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 23:  
US-09-056-285A-23

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5727 CTGGAACCCCAACCCAGGA 5746  
DB 20 CTGGAACCCCAACCCAGGA 1

RESULT 36  
US-09-056-285A-25/c  
Sequence 25, Application US/09056285A  
Patent No. 6403307  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.M.  
Fingert, John  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,285A  
FILING DATE: 07-Apr-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-010.28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 25:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 25:  
US-09-056-285A-25

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5821 AAAATGAGATCTGCCACAG 5840  
DB 20 AAAATGAGATCTGCCACAG 1

RESULT 37  
US-09-056-285A-26  
Sequence 26, Application US/09056285A  
Patent No. 6403307  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.M.  
Fingert, John  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HONG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,285A  
FILING DATE: 07-Apr-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-010,28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 26:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 26:  
US-09-056-285A-26  
Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5791 TGGAGAGAGAGAGAGCA 5810  
DB 1 TGGAGAGAGAGAGAGCA 20  
RESULT 38  
US-09-056-285A-27/c  
Sequence 27, Application US/09056285A  
Patent No. 6403307  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.W.  
Fingert, John  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HONG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,285A  
FILING DATE: 07-Apr-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-010,28  
TELECOMMUNICATION INFORMATION:

TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 27:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 27:  
US-09-056-285A-27  
Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 5958 GGGGACTCTGAGTTGACAG 5977  
DB 20 GGGGACTCTGAGTTGACAG 1  
RESULT 39  
US-09-780-175-25/c  
Sequence 25, Application US/09780175  
Patent No. 6440738  
GENERAL INFORMATION:  
APPLICANT: Robert McKay  
Freier  
APPLICANT: Susan M. Freier  
Jacqueline Wyalt  
TITLE OF INVENTION: ANTISENSE MODULATION OF CASEIN KINASE 2-BETA EXPRESSION  
FILE REFERENCE: RTS-0164  
CURRENT APPLICATION NUMBER: US/09/780,175  
CURRENT FILING DATE: 2001-02-08  
NUMBER OF SEQ ID NOS: 154  
SEQ ID NO 25  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Antisense Oligonucleotide  
US-09-780-175-25  
Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1340 TCTGCTCCGAGGTTCAGC 1359  
DB 20 TCTGCTCCGAGGTTCAGC 1  
RESULT 40  
US-09-607-529-3/c  
Sequence 3, Application US/09607529  
Patent No. 6465247  
GENERAL INFORMATION:  
APPLICANT: Irving Weissman  
David Traver  
APPLICANT: Koichi Akashi  
TITLE OF INVENTION: MAMMALIAN MYELOID PROGENITOR CELL  
FILE REFERENCE: STAN-126  
CURRENT APPLICATION NUMBER: US/09/607,529  
CURRENT FILING DATE: 2000-06-29  
PRIOR APPLICATION NUMBER: 60/141,421  
PRIORITY FILING DATE: 1999-06-29  
NUMBER OF SEQ ID NOS: 6  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 3  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens



US-09-607-529-3

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1511 AGTGTGGATTACAGCAT 1530  
DB 20 AGTGTGGATTACAGCAT 1

RESULT 41  
US-09-306-828-7  
Sequence 7, Application US/09306828  
Patent No. 6475724  
GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
APPLICANT: Chen, Pu  
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And  
CURRENT APPLICATION NUMBER: US/09/306,828  
EARLIER FILING DATE: 1999-05-07  
EARLIER APPLICATION NUMBER: US 09/227,881  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 7  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-828-7

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4955 TGAATCAGCACCCAGTG 4974  
DB 1 TGAATCAGCACCCAGTG 20

RESULT 42  
US-09-306-828-9  
Sequence 9, Application US/09306828  
Patent No. 6475724  
GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
APPLICANT: Chen, Pu  
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And  
CURRENT APPLICATION NUMBER: US/09/306,828  
EARLIER FILING DATE: 1999-05-07  
EARLIER APPLICATION NUMBER: US 09/227,881  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 9  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-828-9

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4587 AGAGTCCCCAGATTACCC 4606  
DB 1 AGAGTCCCCAGATTACCC 20

RESULT 43

US-09-306-828-10/c  
Sequence 10, Application US/09306828  
Patent No. 6475724  
GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
APPLICANT: Chen, Pu  
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis  
CURRENT APPLICATION NUMBER: US/09/306,828  
EARLIER FILING DATE: 1999-05-07  
EARLIER APPLICATION NUMBER: US 09/227,881  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 10  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-828-10

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4581 CTGAGAGAGTCCCCAGAT 4600  
DB 20 CTGAGAGAGTCCCCAGAT 1

RESULT 44  
US-09-306-828-13

Sequence 13, Application US/09306828  
Patent No. 6475724  
GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
APPLICANT: Chen, Pu  
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis  
CURRENT APPLICATION NUMBER: US/09/306,828  
EARLIER FILING DATE: 1999-05-07  
EARLIER APPLICATION NUMBER: US 09/227,881  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 13  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-828-13

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3933 TCAGGCTTAAGTGCAGAAC 3952  
DB 1 TCAGGCTTAAGTGCAGAAC 20

RESULT 45  
US-09-306-828-19

Sequence 19, Application US/09306828  
Patent No. 6475724  
GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
APPLICANT: Chen, Pu  
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis  
CURRENT APPLICATION NUMBER: US/09/306,828

CURRENT FILING DATE: 1999-05-07  
EARLIER APPLICATION NUMBER: US 09/227,881  
EARLIER FILING DATE: 1999-01-11  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 19  
LENGTH: 20  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-306-828-19

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5643 ACCTTGACACGCTGCAG 5662  
DB 1 ACCTTGACACGCTGCAG 20

RESULT 46  
US-09-060-299-257/c  
Sequence 257, Application US/09060299  
Patent No. 6545137  
GENERAL INFORMATION:  
APPLICANT: Todd, John A  
APPLICANT: Hess, John W  
APPLICANT: Caskey, Charles T  
APPLICANT: Cox, Roger D  
APPLICANT: Gerhold, David  
APPLICANT: Hammond, Holly  
APPLICANT: Hey, Patricia  
APPLICANT: Kawaguchi, Yoshihiko  
APPLICANT: Merriman, Tony R  
APPLICANT: Metzker, Michael L  
TITLE OF INVENTION: No. 6545137el Receptor  
NUMBER OF SEQUENCES: 455  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vanderhye  
STREET: 1100 No. 6545137th Glebe Road, Eighth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: US  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/060,299  
FILING DATE: 15-APR-1998  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/043,553  
FILING DATE: 15-APR-1997  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/048,740  
FILING DATE: 05-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: B.J. Sadoff  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 620-35  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4091  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 257:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-09-060-299-257

Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1511 AGTCTGGATTACAGCAT 1530  
DB 20 AGTCTGGATTACAGCAT 1

RESULT 47  
US-09-402-923A-257/c  
Sequence 257, Application US/09402923A  
Patent No. 655654  
GENERAL INFORMATION:  
APPLICANT: Todd, John A  
APPLICANT: Hess, John W  
APPLICANT: Caskey, Charles T  
APPLICANT: Cox, Roger D  
APPLICANT: Gerhold, David  
APPLICANT: Hammond, Holly  
APPLICANT: Hey, Patricia  
APPLICANT: Kawaguchi, Yoshihiko  
APPLICANT: Merriman, Tony R  
APPLICANT: Metzker, Michael L  
TITLE OF INVENTION: No. 655654el LDL-Receptor  
NUMBER OF SEQUENCES: 455  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Nixon and Vanderhye  
STREET: 1100 No. 655654th Glebe Road, Eighth Floor  
CITY: Arlington  
STATE: Virginia  
COUNTRY: US  
ZIP: VA 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.25 (EPO)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/402,923A  
FILING DATE: 14-FEB-2001  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB98/01102  
FILING DATE: 15-APR-1998  
APPLICATION NUMBER: US 60/043,553  
FILING DATE: 15-APR-1997  
APPLICATION NUMBER: US 60/048,740  
FILING DATE: 05-JUN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: B.J. Sadoff  
REGISTRATION NUMBER: 36,663  
REFERENCE/DOCKET NUMBER: 620-81  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703)816-4091  
TELEFAX: (703)816-4100  
INFORMATION FOR SEQ ID NO: 257:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 20 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 257:  
US-09-402-923A-257  
Query Match 0.3%; Score 20; DB 1; Length 20;  
Best Local Similarity 100.0%; Pred. No. 24;  
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1511 AGTCTGGATTACAGCAT 1530  
DB 20 AGTCTGGATTACAGCAT 1

```
RESULT 48
US-08-222-177A-442/C
; Sequence 442, Application US/08222177A
; Patent No. 5562979
; GENERAL INFORMATION:
; APPLICANT: Weber, James L.
; TITLE OF INVENTION: LENGTH POLYMORPHISMS IN
; TITLE OF INVENTION: (dc-da)n (dg-dt)n SEQUENCES AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 460
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Rose & Stevens, S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/222,177A
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/341,562
; FILING DATE: 21-APR-1989
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REGISTRATION NUMBER: 30,492
; REFERENCE/DOCKET NUMBER: 09865,601
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (608) 831-2100
; TELEFAX: (608) 831-2106
; TELEX:
; INFORMATION FOR SEQ ID NO: 442:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-222-177A-442

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

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RESULT 49
US-08-629-939-10
; Sequence 10, Application US/08629939
; Patent No. 5645995
; GENERAL INFORMATION:
; APPLICANT: Kieback, Dirk G.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED
; TITLE OF INVENTION: RISK OF BREAST OR OVARIAN CANCER
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MIOW, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,873
; FILING DATE: 12-APRIL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kit, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: A-6612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHEICAL: NO
; US-08-629-939-10

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/629,939
FILING DATE: 12-APRIL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kit, Gordon
REGISTRATION NUMBER: 30,764
REFERENCE/DOCKET NUMBER: A-6612
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 293-7060
TELEFAX: (202) 293-7860
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
HYPOTHEICAL: NO
US-08-629-939-10

Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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RESULT 50
US-08-759-873-10
; Sequence 10, Application US/08759873
; Patent No. 5683865
; GENERAL INFORMATION:
; APPLICANT: Kieback, Dirk G.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED RISK
; TITLE OF INVENTION: OF BREAST OR OVARIAN CANCER
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MIOW, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,873
; FILING DATE: 12-APRIL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kit, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: A-6612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHEICAL: NO
; US-08-759-873-10
```

```
Query Match      0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
RESULT 51
US-08-759-873-10
; Sequence 10, Application US/08759873
; Patent No. 5683865
; GENERAL INFORMATION:
; APPLICANT: Kieback, Dirk G.
; TITLE OF INVENTION: METHODS FOR DIAGNOSING AN INCREASED RISK
; TITLE OF INVENTION: OF BREAST OR OVARIAN CANCER
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SUGHRUE, MIOW, ZINN, MACPEAK & SEAS
; STREET: 2100 Pennsylvania Avenue, N.W., Suite 800
; CITY: Washington, D.C.
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/759,873
; FILING DATE: 12-APRIL-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Kit, Gordon
; REGISTRATION NUMBER: 30,764
; REFERENCE/DOCKET NUMBER: A-6612
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 293-7060
; TELEFAX: (202) 293-7860
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA
; HYPOTHEICAL: NO
; US-08-759-873-10
```

Query Match 0.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1509 AAGTGTGGATTACAGG 1527  
|||||  
DB 1 AAGTGTGGATTACAGG 19

RESULT 51  
US-08-915-609-3/c  
; Sequence 3, Application US/08915609  
; Patent No. 6054300  
; GENERAL INFORMATION:  
; APPLICANT: McKendree Jr., William L.  
; TITLE OF INVENTION: Single-Site Amplification (SSA) Method for Accelerated  
; FILE REFERENCE: 0115.97  
; CURRENT FILING DATE: 1997-08-21  
; EARLIER APPLICATION NUMBER: 60/028,775  
; EARLIER FILING DATE: 1996-08-23  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO: 3  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; NAME/KEY: primer bind  
; LOCATION: (1)..(19)  
; NAME/KEY: primer bind  
; LOCATION: (1)..(19)  
US-08-915-609-3

Query Match 0.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTG 5014  
|||||  
DB 19 GTGTGTGTGTGTGTGTG 1

RESULT 52  
US-08-915-609-4  
; Sequence 4, Application US/08915609  
; Patent No. 6054300  
; GENERAL INFORMATION:  
; APPLICANT: McKendree Jr., William L.  
; TITLE OF INVENTION: Single-Site Amplification (SSA) Method for Accelerated  
; FILE REFERENCE: 0115.97  
; CURRENT FILING DATE: 1997-08-21  
; EARLIER APPLICATION NUMBER: 60/028,775  
; EARLIER FILING DATE: 1996-08-23  
; NUMBER OF SEQ ID NOS: 6  
; SOFTWARE: PatentIn Ver. 2.0 - beta  
; SEQ ID NO: 4  
; LENGTH: 19  
; TYPE: DNA  
; ORGANISM: Artificial Sequence  
; FEATURE:  
; OTHER INFORMATION: Description of Artificial Sequence: primer  
; NAME/KEY: primer bind  
; LOCATION: (1)..(19)  
; FEATURE:

NAME/KEY: primer bind  
; LOCATION: (1)..(19)  
US-08-915-609-4

Query Match 0.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTG 5014  
|||||  
DB 1 GTGTGTGTGTGTGTGTG 19

RESULT 53  
US-08-938-669A-11  
; Sequence 11, Application US/08938669A  
; Patent No. 6171788  
; GENERAL INFORMATION:  
; APPLICANT: Nguyen, Thai D.  
; TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,  
; TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
; TITLE OF INVENTION: RELATED DISEASES  
; NUMBER OF SEQUENCES: 32  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Howrey & Simon  
; STREET: 1299 Pennsylvania Avenue, N.W.  
; CITY: Washington  
; STATE: DC  
; COUNTRY: USA  
; ZIP: 20004-2402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Diskette  
; COMPUTER: IBM Compatible  
; OPERATING SYSTEM: DOS  
; SOFTWARE: FastSeq for Windows Version 2.0  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/938,669A  
; FILING DATE:  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 08/791,154  
; FILING DATE: 28-JAN-1997  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Mendelson, Elliot  
; REGISTRATION NUMBER: P-42,878  
; REFERENCE/DOCKET NUMBER: 07425-0034  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 202 383-6857  
; TELEFAX: 202 383-6610  
; TELEX:  
; INFORMATION FOR SRO ID NO: 11:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 19 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
US-08-938-669A-11

Query Match 0.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4392 TACAGTTGTGCAGATACG 4410  
|||||  
DB 1 TACAGTTGTGCAGATACG 19

RESULT 54  
US-08-938-669A-14/c  
; Sequence 14, Application US/08938669A  
; Patent No. 6171788  
; GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.  
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
TITLE OF INVENTION: RELATED DISEASES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,669A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/791,154  
FILING DATE: 28-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mendelson, Elliot  
REGISTRATION NUMBER: P-42,878  
REFERENCE/DOCKET NUMBER: 07425-0034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 383-6857  
TELEFAX: 202 383-6610  
TELEX:  
INFORMATION FOR SEQ ID NO: 14:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-938-669A-14  
Query Match 0.3% Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3936 GGCTTAAGTCAGAACCA 3954  
Db 19 GGCTTAAGTCAGAACCA 1  
RESULT 55  
US-08-938-669A-15  
Sequence 15, Application US/08938669A  
Patent No. 6171788  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thai D.  
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
TITLE OF INVENTION: RELATED DISEASES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,669A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/791,154  
FILING DATE: 28-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mendelson, Elliot  
REGISTRATION NUMBER: P-42,878  
REFERENCE/DOCKET NUMBER: 07425-0034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 383-6857  
TELEFAX: 202 383-6610  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-938-669A-15

CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,669A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/791,154  
FILING DATE: 28-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mendelson, Elliot  
REGISTRATION NUMBER: P-42,878  
REFERENCE/DOCKET NUMBER: 07425-0034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 383-6857  
TELEFAX: 202 383-6610  
TELEX:  
INFORMATION FOR SEQ ID NO: 15:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
US-08-938-669A-15  
Query Match 0.3% Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 3727 AACAGACAGAGGCATCC 3745  
Db 1 AACAGACAGAGGCATCC 19  
RESULT 56  
US-08-938-669A-17  
Sequence 17, Application US/08938669A  
Patent No. 6171788  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thai D.  
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
TITLE OF INVENTION: RELATED DISEASES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC  
COUNTRY: USA  
ZIP: 20004-2402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/938,669A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/791,154  
FILING DATE: 28-JAN-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Mendelson, Elliot  
REGISTRATION NUMBER: P-42,878  
REFERENCE/DOCKET NUMBER: 07425-0034  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 202 383-6857  
TELEFAX: 202 383-6610  
TELEX:  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 19 base pairs

TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear

Query Match 0.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5373 CCTGAGATGCCAGCTGTCC 5391  
DB 1 CCTGAGATGCCAGCTGTCC 19

## RESULT 57

US-08-938-669A-22/c  
Sequence 22, Application US/08938669A  
Patent No. 6171788

## GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS  
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
TITLE OF INVENTION: RELATED DISEASES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC

COUNTRY: USA

ZIP: 20004-2402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/938,669A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/791,154

FILING DATE: 28-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mendelson, Elliot

REGISTRATION NUMBER: P-42,878

REFERENCE/DOCKET NUMBER: 07425-0034

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 383-6857

TELEFAX: 202 383-6610

TELEX:

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-938-669A-22

Query Match 0.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5864 GGTAGCAGGCTGAGAGG 5882  
DB 19 GGTAGCAGGCTGAGAGG 1

## RESULT 58

US-08-938-669A-24/c  
Sequence 24, Application US/08938669A  
Patent No. 6171788

## GENERAL INFORMATION:

APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
TITLE OF INVENTION: METHODS FOR THE DIAGNOSIS,  
TITLE OF INVENTION: PROGNOSIS AND TREATMENT OF GLAUCOMA AND  
TITLE OF INVENTION: RELATED DISEASES  
NUMBER OF SEQUENCES: 32  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Howrey & Simon  
STREET: 1299 Pennsylvania Avenue, N.W.  
CITY: Washington  
STATE: DC

COUNTRY: USA

ZIP: 20004-2402

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/938,669A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/791,154

FILING DATE: 28-JAN-1997

ATTORNEY/AGENT INFORMATION:

NAME: Mendelson, Elliot

REGISTRATION NUMBER: P-42,878

REFERENCE/DOCKET NUMBER: 07425-0034

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 383-6857

TELEFAX: 202 383-6610

TELEX:

INFORMATION FOR SEQ ID NO: 24:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-938-669A-24

Query Match 0.3%; Score 19; DB 1; Length 19;  
Best Local Similarity 100.0%; Pred. No. 28;  
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5534 GGCCATGTCAGTCATCAT 5552  
DB 19 GGCCATGTCAGTCATCAT 1

## RESULT 59

US-09-056-285A-19/c  
Sequence 19, Application US/09056285A  
Patent No. 6403307

## GENERAL INFORMATION:

APPLICANT: Stone, Edwin M.  
APPLICANT: Sheffield, Val C.  
APPLICANT: Alward, Wallace L.W.  
APPLICANT: Fingert, John  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: POLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS

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/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA: US/09/056,285A
/ APPLICATION NUMBER: US/09/056,285A
/ FILING DATE: 07-Apr-1998
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Arnold, Beth E.
/   REGISTRATION NUMBER: 35,430
/   REFERENCE/DOCKET NUMBER: UIA-010.28
/ TELECOMMUNICATION INFORMATION:
/   TELEPHONE: 617-832-1000
/   TELEFAX: 617-832-7000
/ INFORMATION FOR SEQ ID NO: 19:
/ SEQUENCE CHARACTERISTICS:
/   LENGTH: 19 base pairs
/   TYPE: nucleic acid
/   STRANDEDNESS: single
/   TOPOLOGY: linear
/ MOLECULE TYPE: other nucleic acid
/ DESCRIPTION: /desc = "primer"
/ SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-056-285A-19

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      5531 CCAGGCCATGTCATC 5549
DB      19 CCAGGCCATGTCATC 1

RESULT 60
US-09-306-828-11
; Sequence 11, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 11
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-11

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      4392 TACAGTTGTCAGATACG 4410
DB      1 TACAGTTGTCAGATACG 19

RESULT 61
US-09-306-828-14/C
; Sequence 14, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
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/ CURRENT FILING DATE: 1999-05-07
/ EARLIER APPLICATION NUMBER: US 09/227,881
/ EARLIER FILING DATE: 1999-01-11
/ NUMBER OF SEQ ID NOS: 38
/ SOFTWARE: Microsoft Word 97
/ SEQ ID NO 14
/ LENGTH: 19
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-306-828-14

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3936 GGCTTACTGCAGAACCA 3954
DB      19 GGCTTACTGCAGAACCA 1

RESULT 62
US-09-306-828-15
; Sequence 15, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 15
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-15

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      3727 AGCAGCACAAGGCAATCC 3745
DB      1 AGCAGCACAAGGCAATCC 19

RESULT 63
US-09-306-828-17
; Sequence 17, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 17
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-17
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Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5373 CCTGAGATCCAGCTGTCC 5391
DB      1 CCTGAGATCCAGCTGTCC 19

RESULT 64
US-09-306-828-22/C
; Sequence 22, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 22
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-22

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5864 GGTACGAGCTGAGAGG 5882
DB      19 GGTACGAGCTGAGAGG 1

RESULT 65
US-09-306-828-24/C
; Sequence 24, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 24
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-24

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5534 GGCATGTCATTCATCCAT 5552
DB      19 GGCATGTCATTCATCCAT 1

RESULT 66
US-09-306-828-35

; Sequence 35, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 35
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-35

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5045 AACTATTATGGCGGTATGG 5063
DB      1 AACTATTATGGCGGTATGG 19

RESULT 67
US-09-306-828-36/C
; Sequence 36, Application US/09306828
; Patent No. 6475724
; GENERAL INFORMATION:
; APPLICANT: Nguyen, Thai D.
; APPLICANT: Polansky, Jon R.
; APPLICANT: Chen, Pu
; APPLICANT: Chen, Hua
; TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis, Prognosis And
; CURRENT APPLICATION NUMBER: US/09/306,828
; CURRENT FILING DATE: 1999-05-07
; EARLIER APPLICATION NUMBER: US 09/227,881
; EARLIER FILING DATE: 1999-01-11
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: Microsoft Word 97
; SEQ ID NO 36
; LENGTH: 19
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-306-828-36

Query Match          0.3%; Score 19; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5309 CCAGAGGAGCCTCACCAG 5327
DB      19 CCAGAGGAGCCTCACCAG 1

RESULT 68
US-08-700-530-1/C
; Sequence 1, Application US/08700530
; Patent No. 6316186
; GENERAL INFORMATION:
; APPLICANT: EKINS, Roger P
; TITLE OF INVENTION: Binding assay using binding agents with tail groups
; FILE REFERENCE: 0380-P01180US0
; CURRENT APPLICATION NUMBER: US/08/700,530
; CURRENT FILING DATE: 1996-10-23
; PRIOR APPLICATION NUMBER: PCT/GB95/00521
; PRIOR FILING DATE: 1995-03-10
; PRIOR APPLICATION NUMBER: GB 9404709.9
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PRIOR FILING DATE: 1994-03-11  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
US-08-700-530-1

Query Match 0.3%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTG 5014  
DB 18 TGTGTGTGTGTGTGTGTG 1

RESULT 69  
US-08-700-530-2  
Sequence 2, Application US/08700530  
Patent No. 6316186  
GENERAL INFORMATION:  
APPLICANT: EKINS, Roger P  
TITLE OF INVENTION: Binding assay using binding agents with tail groups  
FILE REFERENCE: 0380-P0118US9  
CURRENT APPLICATION NUMBER: US/08/700,530  
CURRENT FILING DATE: 1996-10-23  
PRIOR APPLICATION NUMBER: PCT/GB95/00521  
PRIOR FILING DATE: 1995-03-10  
PRIOR APPLICATION NUMBER: GB 9404709.9  
PRIOR FILING DATE: 1994-03-11  
NUMBER OF SEQ ID NOS: 4  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:  
US-08-700-530-2

Query Match 0.3%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGT 5013  
DB 1 GTGTGTGTGTGTGTGTGT 18

RESULT 70  
US-08-976-427-28  
Sequence 28, Application US/08976427A  
Patent No. 6322968  
GENERAL INFORMATION:  
APPLICANT: Head, Steven R.  
APPLICANT: Geoleit, Philip  
APPLICANT: Karn, Jonathan  
APPLICANT: Boyce-Jacino, Michael  
TITLE OF INVENTION: De No. 6322968 or "Universal" Sequencing Array  
FILE REFERENCE: 04990.0049  
CURRENT APPLICATION NUMBER: US/08/976,427A  
CURRENT FILING DATE: 1997-11-21  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: PastSeq for Windows Version 3.0  
SEQ ID NO 28  
LENGTH: 18  
TYPE: DNA

ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic primer  
US-08-976-427-28

Query Match 0.3%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTG 5014  
DB 1 TGTGTGTGTGTGTGTGTG 18

RESULT 71  
US-09-648-312-28  
Sequence 28, Application US/09648312  
Patent No. 6337188  
GENERAL INFORMATION:  
APPLICANT: Head, Steven R.  
APPLICANT: Geoleit, Philip  
APPLICANT: Karn, Jonathan  
APPLICANT: Boyce-Jacino, Michael  
TITLE OF INVENTION: De No. 6337188 or "Universal" Sequencing Array  
FILE REFERENCE: 04990.0049  
CURRENT APPLICATION NUMBER: US/09/648,312  
CURRENT FILING DATE: 2000-08-25  
NUMBER OF SEQ ID NOS: 31  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 28  
LENGTH: 18  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic primer  
US-09-648-312-28

Query Match 0.3%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTG 5014  
DB 1 TGTGTGTGTGTGTGTGTG 18

RESULT 72  
US-09-056-285A-17/c  
Sequence 17, Application US/09056285A  
Patent No. 6403307  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
APPLICANT: Sheffield, Val C.  
APPLICANT: Alward, Wallace L.M.  
Fingert, John  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSER: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,285A  
FILING DATE: 07-Apr-1998  
ATTORNEY/AGENT INFORMATION:

NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-010.28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 17:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 17:  
US-09-056-285A-17

Query Match 0.3%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5372 GCGTGGATGCGAGCTGT 5389  
DB 18 GCGTGGATGCGAGCTGT 1

RESULT 73  
US-09-056-285A-18  
Sequence 18, Application US/09056285A  
Patent No. 6403307  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.M.  
Fingert, John  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,285A  
FILING DATE: 07-Apr-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-010.28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 18:  
US-09-056-285A-18

Query Match 0.3%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5354 ACCTGCTGCGAGCTTGG 5371  
DB 1 ACCTGCTGCGAGCTTGG 18

RESULT 74  
US-09-056-285A-24  
Sequence 24, Application US/09056285A  
Patent No. 6403307  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
Sheffield, Val C.  
Alward, Wallace L.M.  
Fingert, John  
TITLE OF INVENTION: GLAUCOMA THERAPEUTICS AND DIAGNOSTICS  
NUMBER OF SEQUENCES: 43  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: FOLEY, HOAG & ELIOT LLP  
STREET: One Post Office Square  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02109-2170  
COMPUTER READABLE FORM:  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/056,285A  
FILING DATE: 07-Apr-1998  
ATTORNEY/AGENT INFORMATION:  
NAME: Arnold, Beth E.  
REGISTRATION NUMBER: 35,430  
REFERENCE/DOCKET NUMBER: UIA-010.28  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-832-1000  
TELEFAX: 617-832-7000  
INFORMATION FOR SEQ ID NO: 24:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 18 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
DESCRIPTION: /desc = "primer"  
SEQUENCE DESCRIPTION: SEQ ID NO: 24:  
US-09-056-285A-24

Query Match 0.3%; Score 18; DB 1; Length 18;  
Best Local Similarity 100.0%; Pred. No. 32;  
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5641 TGACCTTGACGAGGCTG 5638  
DB 1 TGACCTTGACGAGGCTG 18

RESULT 75  
US-08-222-177A-448/C  
Sequence 448, Application US/08222177A  
Patent No. 5582979  
GENERAL INFORMATION:  
APPLICANT: Weber, James L.  
TITLE OF INVENTION: LENGTH POLYMORPHISMS IN  
SEQUENCES AND METHODS OF USING SAME  
NUMBER OF SEQUENCES: 460  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Demilt Ross & Stevens, S.C.  
STREET: 8000 Excelsior Drive, Suite 401  
CITY: Madison  
STATE: Wisconsin

COUNTRY: USA  
ZIP: 53717-1914  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/222,177A  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/341,562  
FILING DATE: 21-APR-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: Sara, Charles S.  
REGISTRATION NUMBER: 30,492  
REFERENCE/DOCKET NUMBER: 09865,601  
TELEPHONE: (608) 831-2100  
TELEFAX: (608) 831-2106  
TELEX:  
INFORMATION FOR SEQ ID NO: 448:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-08-222-177A-448

Query Match 0.3%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGT 5013  
DB 17 TGTGTGTGTGTGTGTGT 1

RESULT 76  
US-08-885-126-9  
Sequence 9, Application US/08885126A  
Patent No. 5955597  
GENERAL INFORMATION:  
APPLICANT: Arnold, Lyle J.  
APPLICANT: Riley, Timothy A.  
APPLICANT: Reynolds, Mark A.  
APPLICANT: Schwartz, David A.  
TITLE OF INVENTION: CHIRALLY ENRICHED SYNTHETIC PHOSPHATE  
FILE REFERENCE: GENTA.020FW2  
CURRENT APPLICATION NUMBER: US/08/885,126A  
CURRENT FILING DATE: 1997-06-30  
EARLIER APPLICATION NUMBER: 08/343,018  
EARLIER FILING DATE: 1994-11-21  
EARLIER APPLICATION NUMBER: 08/154,013  
EARLIER FILING DATE: 1993-11-16  
NUMBER OF SEQ ID NOS: 22  
SOFTWARE: FastSeq for Windows Version 3.0  
SEQ ID NO 9  
LENGTH: 17  
TYPE: DNA  
ORGANISM: Artificial Sequence  
OTHER INFORMATION: Chemically synthesized oligomer  
US-08-885-126-9

Query Match 0.3%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5008 GTGTGTGTGTGTGTGT 5024  
DB 1 GTGTGTGTGTGTGTGT 1

DB 1 GTGTGTGTGTGTGTGT 17

RESULT 77  
US-08-960-111-11  
Sequence 11, Application US/08960111  
Patent No. 6060456  
GENERAL INFORMATION:  
APPLICANT: Arnold Jr., Lyle J  
APPLICANT: Reynolds, Mark A  
APPLICANT: Giachetti, Christina  
TITLE OF INVENTION: Chimeric Oligonucleoside Compounds  
NUMBER OF SEQUENCES: 27  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Lyon & Lyon  
STREET: 611 West Sixth St.  
CITY: Los Angeles  
STATE: CA  
COUNTRY: U.S.A.  
ZIP: 90017  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/960,111  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/238,177  
FILING DATE: 04-MAY-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Meier, Paul H.  
REGISTRATION NUMBER: 32,274  
REFERENCE/DOCKET NUMBER: 207/174  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 213/489-1600  
TELEFAX: 213/955-0440  
TELEX: 67-3510  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 17 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: other nucleic acid  
HYPOTHECTICAL: no  
ANTI-SENSE: yes  
FEATURE:  
NAME/KEY: GT oligomers 2517-1, 2516-1  
IDENTIFICATION METHOD: synthesis experiments  
OTHER INFORMATION: complementary to synthetic RNA  
OTHER INFORMATION: target  
US-08-960-111-11

Query Match 0.3%; Score 17; DB 1; Length 17;  
Best Local Similarity 100.0%; Pred. No. 37;  
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5008 GTGTGTGTGTGTGTGT 5024  
DB 1 GTGTGTGTGTGTGTGT 17

RESULT 78  
US-09-490-774-11  
Sequence 11, Application US/09490774  
Patent No. 6262036  
GENERAL INFORMATION:  
APPLICANT: Arnold Jr., Lyle J  
APPLICANT: Reynolds, Mark A

```

APPLICANT: Giachetti, Christina
TITLE OF INVENTION: Chimeric Oligonucleoside Compounds
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Lyon & Lyon
STREET: 611 West Sixth St.
CITY: Los Angeles
STATE: CA
COUNTRY: U.S.A.
ZIP: 90017

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,774
FILING DATE:

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/960,111
FILING DATE:
APPLICATION NUMBER: US/08/238,177
FILING DATE: 04-MAY-1994
ATTORNEY/AGENT INFORMATION:
NAME: Meier, Paul H.
REGISTRATION NUMBER: 32,274
REFERENCE/DOCKET NUMBER: 207/174
TELECOMMUNICATION INFORMATION:
TELEPHONE: 213/489-1600
TELEFAX: 213/955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: no
ANTI-SENSE: yes
FEATURE:
NAME/KEY: GT oligomers 2517-1, 2516-1
IDENTIFICATION METHOD: synthesis experiments
OTHER INFORMATION: complementary to synthetic RNA
OTHER INFORMATION: target
US-09-490-774-11
Query Match 0.3% Score 17; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Search completed: September 23, 2004, 09:57:15  
Job time : 6 secs

Qy	5008	GTGTGTGTGTGTGTA	5024
Db	1	GTGTGTGTGTGTGTA	17

GenCore version 5.1.6  
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ALIGNMENTS

OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 09:58:51; Search time 4 Seconds

(without alignments)  
2.952 Million cell updates/sec

Title: US-09-227-881-3

Sequence: 1 accttgcagttacac.....ctgtgcacccatgcag 6169

Scoring table: IDENTITY\_NUC

Gapop 10.0, Gapext 0.5

Searched: 32 segs, 957 residues

Total number of hits satisfying chosen parameters: 64

Minimum DB seq length: 12

Maximum DB seq length: 250

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 33 summaries

Database: rnpb3.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	3.7	227	1	US-10-244-633-38
2	32	0.5	32	1	US-10-017-870-1
3	29	0.5	29	1	US-09-952-464-11
4	27	0.4	27	1	US-09-735-363A-1
5	27	0.4	27	1	US-09-735-363A-5
6	27	0.4	27	1	US-09-735-363A-66
7	27	0.4	27	1	US-09-263-959-770
8	27	0.4	27	1	US-10-168-327-2
9	24	0.4	24	1	US-09-735-363A-21
10	24	0.4	24	1	US-09-735-363A-22
11	24	0.4	24	1	US-09-776-479-1068
12	24	0.4	24	1	US-09-776-479-1068
13	24	0.4	24	1	US-09-909-317-6
14	24	0.4	24	1	US-10-314-578-1068
15	24	0.4	24	1	US-10-112-653-1012
16	24	0.4	24	1	US-10-017-995-1068
17	24	0.4	24	1	US-10-374-307-7
18	24	0.4	24	1	US-10-374-307-12
19	24	0.4	24	1	US-10-244-633-38
20	21	0.3	21	1	US-09-735-363A-19
21	21	0.3	21	1	US-09-735-363A-20
22	21	0.3	21	1	US-09-776-479-907
23	21	0.3	21	1	US-09-776-479-907
24	21	0.3	21	1	US-09-985-637A-4
25	21	0.3	21	1	US-09-985-637A-8
26	21	0.3	21	1	US-10-314-578-907
27	21	0.3	21	1	US-10-112-653-876
28	21	0.3	21	1	US-10-017-995-907
29	21	0.3	21	1	US-10-244-633-8
30	21	0.3	21	1	US-10-244-633-12
31	21	0.3	21	1	US-10-287-226-567
32	21	0.3	21	1	US-10-741-339-4
33	21	0.3	21	1	US-10-741-339-8

QY	5045	AACTATTATGGGGGATGAGGATGATTAATTTCTTAAGATCTGTGTCAGCGGAAGGCAACCCCTG	5104
DB	1	AACTATTATGGGGGATGAGGATGATTAATTTCTTAAGATCTGTGTCAGCGGAAGGCAACCCCTG	60
QY	5105	CGACTCTGGAAGGATTTCTTAAGATCTGTGTCAGCGGAAGGCAACCCCTG	5164
DB	61	CGACTCTGGAAGGATTTCTTAAGATCTGTGTCAGCGGAAGGCAACCCCTG	120
QY	5165	TGCACAGCCCAACCAAGCCTCAAGTGCACCTCTGTCTTCCCATGAGGGCTGCTC	5224
DB	121	TGCACAGCCCAACCAAGCCTCAAGTGCACCTCTGTCTTCCCATGAGGGCTGCTC	180
QY	5225	CCAGATATATTAACCTCTGAGCTCGGCGATGAGCCAGCAAG	5271
DB	181	CCAGATATATTAACCTCTGAGCTCGGCGATGAGCCAGCAAG	227
RESULT 2			
US-10-017-870-1			
Sequence 1, Application US/10017870			
Publication No. US20030165857A1			
GENERAL INFORMATION:			
APPLICANT: HUMING, DOUG HUI			
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TIGR GENOTYPING ASSAYS			
FILE REFERENCE: 034827-1401			
CURRENT APPLICATION NUMBER: US/10/017,870			
CURRENT FILING DATE: 2001-12-12			
NUMBER OF SEQ ID NOS: 14			
SOFTWARE: PatentIn Ver. 2.1			
SEQ ID NO 1			
LENGTH: 32			
TYPE: DNA			
ORGANISM: Artificial Sequence			
FEATURE:			
OTHER INFORMATION: Description of Artificial Sequence: Primer			
US-10-017-870-1			

Query Match 0.5%; Score 32; DB 1; Length 32;  
Best Local Similarity 100.0%; Pred. No. 2.5;  
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4305 CGAATGAGCCCTAAGTCAAGTGTATATA 4336  
1 CGAATGAGCCCTAAGTCAAGTGTATATA 32

## RESULT 3

US-09-952-464A-11  
Sequence 11, Application US/09952464A  
Publication No. US2003007587A1  
GENERAL INFORMATION:  
APPLICANT: Stone, Edwin M.  
APPLICANT: Sheffield, Val C.  
APPLICANT: Alward, Wallace L.M.  
APPLICANT: Fingert, John  
TITLE OF INVENTION: GLUCOCMA THERAPEUTICS AND DIAGNOSTICS  
FILE REFERENCE: 21087, 0017011  
CURRENT APPLICATION NUMBER: US/09/952,464A  
CURRENT FILING DATE: 2001-09-12  
PRIOR APPLICATION NUMBER: 09/473,273  
PRIOR FILING DATE: 1999-12-28  
PRIOR APPLICATION NUMBER: 09/461,542  
PRIOR FILING DATE: 1999-12-15  
PRIOR APPLICATION NUMBER: 09/366,952  
PRIOR FILING DATE: 1999-08-04  
PRIOR APPLICATION NUMBER: 09/056,285  
PRIOR FILING DATE: 1998-04-07  
PRIOR APPLICATION NUMBER: 08/822,999  
PRIOR FILING DATE: 1997-03-21  
NUMBER OF SEQ ID NOS: 43  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 11  
LENGTH: 29  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence, No. US2003007587A1 =  
US-09-952-464A-11

Query Match 0.5%; Score 29; DB 1; Length 29;  
Best Local Similarity 100.0%; Pred. No. 4.2;  
Matches 29; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5680 AGGGGCTGCAGAGGAGCTGGGACCCCTG 5708  
1 AGGGGCTGCAGAGGAGCTGGGACCCCTG 29

US-09-735-363A-1  
Sequence 1, Application US/09735363A  
Patent No. US20010041681A1  
GENERAL INFORMATION:

APPLICANT: Filion, Mario  
APPLICANT: Phillip, Nigel  
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
FILE REFERENCE: 02811-0181  
CURRENT APPLICATION NUMBER: US/09/735,363A  
CURRENT FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/170,325  
PRIOR FILING DATE: 1999-12-13  
PRIOR APPLICATION NUMBER: 60/228,925  
PRIOR FILING DATE: 2000-08-29  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 1  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence

FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-1

Query Match 0.4%; Score 27; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGTG 5022  
1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTG 27

## RESULT 5

US-09-735-363A-5  
Sequence 5, Application US/09735363A  
Patent No. US20010041681A1  
GENERAL INFORMATION:  
APPLICANT: Filion, Mario  
APPLICANT: Phillip, Nigel  
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
FILE REFERENCE: 02811-0181  
CURRENT APPLICATION NUMBER: US/09/735,363A  
CURRENT FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/170,325  
PRIOR FILING DATE: 1999-12-13  
PRIOR APPLICATION NUMBER: 60/228,925  
PRIOR FILING DATE: 2000-08-29  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 5  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-5

Query Match 0.4%; Score 27; DB 1; Length 27;  
Best Local Similarity 100.0%; Pred. No. 5.7;  
Matches 27; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5023  
1 TGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27

US-09-735-363A-66  
Sequence 66, Application US/09735363A  
Patent No. US20010041681A1  
GENERAL INFORMATION:

APPLICANT: Filion, Mario  
APPLICANT: Phillip, Nigel  
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
FILE REFERENCE: 02811-0181  
CURRENT APPLICATION NUMBER: US/09/735,363A  
CURRENT FILING DATE: 2000-12-12  
PRIOR APPLICATION NUMBER: 60/170,325  
PRIOR FILING DATE: 1999-12-13  
PRIOR APPLICATION NUMBER: 60/228,925  
PRIOR FILING DATE: 2000-08-29  
NUMBER OF SEQ ID NOS: 87  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 66  
LENGTH: 27  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Synthetic Oligonucleotide  
US-09-735-363A-66

Query Match 0.4%; Score 27; DB 1; Length 27;

ORGANISM: Artificial Sequence  
FEATURE:





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APPLICANT: Kronick, Mel N.
TITLE OF INVENTION: METHODS AND DEVICES FOR DETECTING
TITLE OF INVENTION: PRITHREAD MISALIGNMENT OF AN IN SITU POLYMERIC ARRAY
TITLE OF INVENTION: SYNTHESIS DEVICE
FILE REFERENCE: AGIL-078
CURRENT APPLICATION NUMBER: US/10/374,307
CURRENT FILING DATE: 2003-02-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 24
TYPE: DNA
ORGANISM: Homo sapien
US-10-374-307-7

Query Match
Best Local Similarity 100.0%; Score 24; DB 1; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5019
DB GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

RESULT 16
US-10-374-307-12
Sequence 12, Application US/10374307
Publication No. US20040170984A1
GENERAL INFORMATION:
APPLICANT: Leproust, Eric M.
APPLICANT: Amorese, Douglas A.
APPLICANT: Kronick, Mel N.
TITLE OF INVENTION: METHODS AND DEVICES FOR DETECTING
TITLE OF INVENTION: PRINTHREAD MISALIGNMENT OF AN IN SITU POLYMERIC ARRAY
FILE REFERENCE: AGIL-078
CURRENT APPLICATION NUMBER: US/10/374,307
CURRENT FILING DATE: 2003-02-25
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12
LENGTH: 24
TYPE: DNA
ORGANISM: Homo sapien
US-10-374-307-12

Query Match
Best Local Similarity 100.0%; Score 24; DB 1; Length 24;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

CY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 5019
DB GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 24

RESULT 19
US-10-244-633-38/C
Sequence 38, Application US/10244633
Publication No. US20030068640A1
GENERAL INFORMATION:
APPLICANT: Nguyen, Thai D.
APPLICANT: Polansky, Jon R.
APPLICANT: Chen, Hua
APPLICANT: Chen, Pu
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,
TITLE OF INVENTION: Prognosis And Treatment Of Glaucoma And Related
TITLE OF INVENTION: Disorders
FILE REFERENCE: 07425.0057.US01
CURRENT APPLICATION NUMBER: US/10/244,633
CURRENT FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: US/09/306,828
PRIOR FILING DATE: 1999-05-07
PRIOR APPLICATION NUMBER: US 09/227,881

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/ PRIOR FILING DATE: 1999-01-11  
 / NUMBER OF SEQ ID NOS: 38  
 / SOFTWARE: Microsoft Word 97  
 / SEQ ID NO 38  
 / LENGTH: 227  
 / TYPE: DNA  
 / ORGANISM: Homo sapiens  
 / US-10-244-633-38

Query Match 0.4%; Score 22.4; DB 1; Length 227;  
 Best Local Similarity 81.2%; Pred. No. 7.4;  
 Matches 26; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 5073 TTGGAGTGTCTTTTAAAGAACTCCAA 5104  
 DB 60 TTGGAGTGTCTTTTAAAGAACTCCAA 29

RESULT 20  
 / US-09-735-363A-19  
 / Sequence 19, Application US/09735363A  
 / Patent No. US20010041681A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Phillip, Mario  
 / TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
 / FILE REFERENCE: 02811-0181  
 / CURRENT APPLICATION NUMBER: US/09/735,363A  
 / PRIOR FILING DATE: 2000-12-12  
 / PRIOR APPLICATION NUMBER: 60/170,325  
 / PRIOR FILING DATE: 1999-12-13  
 / PRIOR APPLICATION NUMBER: 60/226,925  
 / NUMBER OF SEQ ID NOS: 87  
 / SOFTWARE: Patent version 3.0  
 / SEQ ID NO 19  
 / LENGTH: 21  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic Oligonucleotide  
 / US-09-735-363A-19

Query Match 0.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGT 5017  
 DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 21

RESULT 21  
 / US-09-735-363A-20  
 / Sequence 20, Application US/09735363A  
 / Patent No. US20010041681A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Fillion, Mario  
 / TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides  
 / FILE REFERENCE: 02811-0181  
 / CURRENT APPLICATION NUMBER: US/09/735,363A  
 / PRIOR FILING DATE: 2000-12-12  
 / PRIOR APPLICATION NUMBER: 60/170,325  
 / PRIOR FILING DATE: 1999-12-13  
 / PRIOR APPLICATION NUMBER: 60/226,925  
 / NUMBER OF SEQ ID NOS: 87  
 / SOFTWARE: Patent version 3.0  
 / SEQ ID NO 20  
 / LENGTH: 21  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence

/ FEATURE:  
 / OTHER INFORMATION: Synthetic Oligonucleotide  
 / US-09-735-363A-20

Query Match 0.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4996 GTGTGTGTGTGTGTGTGTGTGTGTGTG 5016  
 DB 1 GTGTGTGTGTGTGTGTGTGTGTGTGTG 21

RESULT 22  
 / US-09-776-479-907  
 / Sequence 907, Application US/09776479  
 / Publication No. US20030087848A1  
 / GENERAL INFORMATION:  
 / APPLICANT: Bratzler, Robert L.  
 / APPLICANT: Petersen, Deanna M.  
 / TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
 / FILE REFERENCE: C1037/7013 (HCL/MAT)  
 / CURRENT APPLICATION NUMBER: US/09/776,479  
 / PRIOR FILING DATE: 2001-02-02  
 / PRIOR APPLICATION NUMBER: US 60/179,991  
 / PRIOR FILING DATE: 2000-02-03  
 / NUMBER OF SEQ ID NOS: 1093  
 / SOFTWARE: FastSeq for Windows Version 3.0  
 / SEQ ID NO 907  
 / LENGTH: 21  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic Sequence  
 / US-09-776-479-907

Query Match 0.3%; Score 21; DB 1; Length 21;  
 Best Local Similarity 100.0%; Pred. No. 14;  
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4997 TGTGTGTGTGTGTGTGTGTGTGTGTGT 5017  
 DB 1 TGTGTGTGTGTGTGTGTGTGTGTGTGT 21

RESULT 23  
 / US-09-776-479-907  
 / Sequence 907, Application US/09776479  
 / Publication No. US20040067902A9  
 / GENERAL INFORMATION:  
 / APPLICANT: Bratzler, Robert L.  
 / APPLICANT: Petersen, Deanna M.  
 / TITLE OF INVENTION: Immunostimulatory Nucleic Acids for the  
 / FILE REFERENCE: C1037/7013 (HCL/MAT)  
 / CURRENT APPLICATION NUMBER: US/09/776,479  
 / PRIOR FILING DATE: 2001-02-02  
 / PRIOR APPLICATION NUMBER: US 60/179,991  
 / PRIOR FILING DATE: 2000-02-03  
 / NUMBER OF SEQ ID NOS: 1093  
 / SOFTWARE: FastSeq for Windows Version 3.0  
 / SEQ ID NO 907  
 / LENGTH: 21  
 / TYPE: DNA  
 / ORGANISM: Artificial Sequence  
 / FEATURE:  
 / OTHER INFORMATION: Synthetic Sequence  
 / US-09-776-479-907

Query Match 0.3%; Score 21; DB 1; Length 21;

RESULT 26  
US-10-314-578-907  
; Sequence 907, Application US/10314578  
; Publication No. US20030212026A1  
; GENERAL INFORMATION:

RESULT 28  
 US-10-017-995-907  
 ; Sequence 907, Application US/10017995  
 ; Publication No. US20030055014A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Bratzler, Robert L.  
 ; TITLE OF INVENTION: Inhibition of Angiogenesis by Nucleic Acids  
 ; FILE REFERENCE: C1037/7705 (HCL/WAT)



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; PRIOR FILING DATE: 2002-02-27
; PRIOR APPLICATION NUMBER: 60/364,000
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/404,821
; PRIOR FILING DATE: 2002-08-20
; PRIOR APPLICATION NUMBER: 60/334,526
; PRIOR FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 60/354,409
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: 60/364,227
; PRIOR FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: 60/334,027
; PRIOR FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: 60/331,641
; PRIOR FILING DATE: 2001-11-20
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 673
; SOFTWARE: CuraseqList version 0.1
; SEQ ID NO 567
; LENGTH: 21
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Primer/Probe
US-10-287-226-567

Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 AACTCCTGACCTCAGGTGATC 21

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RESULT 32
US-10-741-339-4/c
; Sequence 4, Application US/10741339
; Publication No. US20040132795A1
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PRO
; FILE REFERENCE: 13587.375
; CURRENT APPLICATION NUMBER: US/10/741,339
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 09/985,637
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4
; LENGTH: 21
; TYPE: DNA
; ORGANISM: synthetic
US-10-741-339-4

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Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 CTATTATGGGGTATGGTGC 1

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RESULT 33
US-10-741-339-8/c
; Sequence 8, Application US/10741339
; Publication No. US20040132795A1
; GENERAL INFORMATION:
; APPLICANT: Polansky, Jon
; TITLE OF INVENTION: METHODS TO SCREEN AND TREAT INDIVIDUALS WITH GLAUCOMA OR THE PRO
; TITLE OF INVENTION: TO DEVELOP GLAUCOMA

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; FILE REFERENCE: 13587.375
; CURRENT APPLICATION NUMBER: US/10/741,339
; CURRENT FILING DATE: 2003-12-22
; PRIOR APPLICATION NUMBER: US 09/985,637
; PRIOR FILING DATE: 2001-11-05
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 21
; TYPE: DNA
; ORGANISM: synthetic
US-10-741-339-8

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Query Match
Best Local Similarity 100.0%; Pred. No. 14;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 21 CAGTGTGCGAGATACGTTGT 1

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Thu Sep 23 10:01:07 2004

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Page 1

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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 10:00:21; Search time 2 seconds  
(without alignments)  
3.788 Million cell updates/sec

Title: US-09-227-881-3

Perfect score: 6169  
Sequence: 1 attctgttcagttacatc.....cttgcccccatgacag 6169

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 0.5

Searched: 4 segs, 614 residues

Total number of hits satisfying chosen parameters: 8

Minimum DB seq length: 12

Maximum DB seq length: 250

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 4 summaries

Database: rnps3.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	227	3.7	227	US-10-244-633-38	Sequence 38, Appl
2	129	2.1	129	US-09-075-126-3026	Sequence 3026, Ap
3	129	2.1	129	US-09-540-208-11923	Sequence 11923, A
4	129	2.1	129	US-60-048-726-3026	Sequence 3026, Ap

#### ALIGNMENTS

RESULT 1  
US-10-244-633-38  
Sequence 38, Application US/10244633  
GENERAL INFORMATION:  
APPLICANT: Nguyen, Thai D.  
APPLICANT: Polansky, Jon R.  
APPLICANT: Chen, Hu  
TITLE OF INVENTION: Nucleic Acids, Kits, And Methods For The Diagnosis,  
Title Of Invention: Prognosis And Treatment Of Glioma And Related  
TITLE OF INVENTION: Disorders  
FILE REFERENCE: 07425.0057.US01  
CURRENT APPLICATION NUMBER: US/10/244,633  
CURRENT FILING DATE: 2002-09-17  
PRIOR APPLICATION NUMBER: US/09/306,828  
PRIOR FILING DATE: 1999-05-07  
PRIOR APPLICATION NUMBER: US 09/227,881  
PRIOR FILING DATE: 1999-01-11  
NUMBER OF SEQ ID NOS: 38  
SOFTWARE: Microsoft Word 97  
SEQ ID NO 38  
LENGTH: 227  
TYPE: DNA  
ORGANISM: Homo sapiens

US-10-244-633-38

Query Match 3.7%; Score 227; DB 1; Length 227;  
Best Local Similarity 100.0%; Pred. No. 0.21;  
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5045 AACTATTATGGGGATGGGTCATPAATGGGATGTTCTTTTAAAGAACTCCAAA 5104  
DB 1 AACTATTATGGGGATGGGTCATPAATGGGATGTTCTTTTAAAGAACTCCAAA 60  
QY 5105 CAGACTTCTGGAAGGTTATTTTCTAAGATCTTGCTGACCGCTGAGAGCAACCCCTG 5164  
DB 61 CAGACTTCTGGAAGGTTATTTTCTAAGATCTTGCTGACCGCTGAGAGCAACCCCTG 120  
QY 5165 TGCACAGCCCCCAGCCCTCAGTGGCCACCTGCTTCCCATGAGGGCTGGCTC 5224  
DB 121 TGCACAGCCCCCAGCCCTCAGTGGCCACCTGCTTCCCATGAGGGCTGGCTC 180  
QY 5225 CCCAGTATATATAAACCCTCTGAGACTGCGGCATGAGCCAGCAAG 5271  
DB 181 CCCAGTATATATAAACCCTCTGAGACTGCGGCATGAGCCAGCAAG 227

RESULT 2  
US-09-075-126-3026  
Sequence 3026, Application US/09075126  
GENERAL INFORMATION:  
APPLICANT: Gooding, Douglas H.  
APPLICANT: Stuve, Laura L.  
APPLICANT: Stuart, Susan G.  
APPLICANT: Ito, Laura Y.  
APPLICANT: Akersblom, Ingrid B.  
APPLICANT: Delegeane, Angelo M.  
APPLICANT: Naughton, Rebecca E.  
APPLICANT: Klingler, Tod M.  
TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES DERIVED FROM  
TITLE OF INVENTION: HUMAN PENIS  
NUMBER OF SEQUENCES: 3727  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: INCYTE PHARMACEUTICALS, INC.  
STREET: 3174 PORTER DRIVE  
CITY: PALO ALTO  
STATE: CALIFORNIA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/075,126  
FILING DATE: HERewith  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: CERONE, MICHAEL C.  
REGISTRATION NUMBER: 39,132  
REFERENCE/DOCKET NUMBER: PD-0375P  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (415) 855-0555  
TELEFAX: (415) 845-4166  
INFORMATION FOR SEQ ID NO: 3026:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 129 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
IMMEDIATE SOURCE:  
CLONE: 3207049H1  
US-09-075-126-3026  
Query Match 2.1%; Score 129; DB 1; Length 129;

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OM nucletic - nucletic search, using sw model  
Run on: September 23, 2004, 09:53:56 : Search time 4 seconds  
(without alignments)  
3.637 Million cell updates/second

Title: US-09-227-881-3  
Perfect score: 6169  
Sequence: 1 atcttgttcagtttaactc.....cttgtycccccctcaatgtcag 6169

Scoring table: IDENTITY\_NUC

Searched: 30 seqs, 1179 residues

Total number of hits satisfying chosen parameters: 60

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Minimum DB seq length: 12
Maximum DB seq length: 250
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Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 32 summaries

Database : rge3.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	227	3.7	227	1	BD237965	ACCESSION:BD237965
2	227	3.7	227	1	AR242775	ACCESSION:AR242775
3	29	0.5	29	1	AR163703	ACCESSION:AR163703
4	29	0.5	29	1	AR212952	ACCESSION:AR212952
5	29	0.5	29	1	BD009314	ACCESSION:BD009314
6	29	0.5	29	1	BD252254	ACCESSION:BD252254
7	28	0.5	28	1	131539	ACCESSION:131539
8	27	0.4	27	1	AR051255	ACCESSION:AR051255
9	27	0.4	27	1	AR127802	ACCESSION:AR127802
10	27	0.4	27	1	128384	ACCESSION:128384
11	27	0.4	27	1	131231	ACCESSION:131231
12	27	0.4	27	1	AX175237	ACCESSION:AX175237
13	27	0.4	27	1	AX175241	ACCESSION:AX175241
14	27	0.4	27	1	AX175300	ACCESSION:AX175300
15	27	0.4	27	1	AX189457	ACCESSION:AX189457
16	26	0.4	26	1	BD103417	ACCESSION:BD103417
17	26	0.4	26	1	BD176939	ACCESSION:BD176939
18	25	0.4	25	1	131234	ACCESSION:131234
19	25	0.4	25	1	AX115976	ACCESSION:AX115976
20	25	0.4	25	1	AX117836	ACCESSION:AX117836
21	25	0.4	25	1	BD103418	ACCESSION:BD103418
22	25	0.4	25	1	BD176940	ACCESSION:BD176940
23	25	0.4	25	1	131533	ACCESSION:131533
24	24	0.4	24	1	AX104876	ACCESSION:AX104876
25	24	0.4	24	1	AX175257	ACCESSION:AX175257
26	24	0.4	24	1	AX175255	ACCESSION:AX175255
27	24	0.4	24	1	AX547929	ACCESSION:AX547929
28	23	0.4	23	1	AR127801	ACCESSION:AR127801
29	23	0.4	23	1	131542	ACCESSION:131542
30	22.4	0.4	227	1	BD237965	ACCESSION:BD237965
31	22.4	0.4	227	1	AR242775	ACCESSION:AR242775
32	22	0.4	22	1	131213	ACCESSION:131213

## ALIGNMENTS

RESULT 1	LOCUS	DEFINITION	ACCESION	VERSION	KEYWORDS	SOURCE	ORGANISM
BD237965	BD237965	227 bp DNA linear	BD237965	BD237965	Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders.	CP 2002S3413-A/32	Homo sapiens (human)

REFERENCE 1 (bases 1 to 227)

**AUTHORS** Nguyen, I. D., Polansky, J. K., Chen, P., and Chen, A.  
**TITLE** Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glioma and related disorders  
**JOURNAL** Patent: JP 2002534135-A 32 15-OCT-2002;  
THIS DOCUMENT IS THE PROPERTY OF CALTECH AND IS LOANED TO THE UNIVERSITY OF CALIFORNIA

COMMENT	OS	Homo sapiens (human)
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PD 15-OCT-2002 TD 000003777

PR 11-JAN-1999 US 09/227881,07-MAY-1999 US 09/306828 P1  
WU T D NGUYEN TON B DO LANSKY PH CHEN HUA CHEN PC

C12N15/09, A61K31/573, A61K45/00, A61P27/06, C12N1/15, C12N1/19, C12N1/21

PC C12N5/10, C12Q1/68, G01N33/53, G01N33/566, C12N15/00, C12N5/00 CC  
 Multiple acids and methods for the diagnosis, prognosis CC

## CC treatment of glaucoma and related disorders and

PH	Key	Location/Qualifiers
ET	source	1. 227

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Db 181 CCAGTATATAAACCCTCTCTGGAGCTCGGGCATGAGCCAGCAAGG 227

RESOL 2  
AR242775

LOCUS 21 25  
DEFINITION Sequence 38 from patent US 6475724.

RECESSION AR242775.1 GI:27289414  
VERSION

SOURCE	Unknown.	1
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Unclassified.  
REFERENCE 1 (bases 1 to 227)  
AUTHORS Nguyen,T.D., Polansky,J.R., Chen,P. and Chen,H.  
TITLE Nucleic acids, kits, and methods for the diagnosis, prognosis and treatment of glaucoma and related disorders  
JOURNAL Patent: US 6475724-A 38 05-NOV-2002;  
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QY 5165 TGCACAGCCGCCACCCAGCCTCAAGTGCACCTCTGTCTTCCCATGAAGGGCTGCTC 5224  
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DB 181 CCAGATATATTAACCTCTCTGAGCTCGGGCATGAGCCAGAG 227

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DEFINITION Sequence 8 from patent US 6271026.  
ACCESSION AR163703  
VERSION AR163703.1 GI:16234393  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Stone,E.M., Sheffield,V.C. and Alward,W.L.M.  
TITLE Glaucoma compositions  
JOURNAL Patent: US 6271026-A 8 07-AUG-2001;  
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LOCUS AR212952 29 bp DNA linear PAT 25-SEP-2002  
DEFINITION Sequence 11 from patent US 6403307.  
ACCESSION AR212952  
VERSION AR212952.1 GI:23309837  
KEYWORDS Unknown.  
SOURCE Unknown.  
ORGANISM Unknown.  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Stone,E.M., Sheffield,V.C., Alward,W.L.M. and Fingert,J.  
TITLE Glaucoma therapeutics and diagnostics

JOURNAL Patent: US 6403307-A 11 11-JUN-2002;  
FEATURES Location/Qualifiers  
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DEFINITION Glaucoma-associated protein and corresponding nucleic acid and their therapeutic and diagnostic uses.  
ACCESSION BD009314  
VERSION BD009314.1 GI:18637687  
KEYWORDS JP 2001503631-A/7.  
SOURCE unidentified  
ORGANISM unidentified  
REFERENCE 1 (bases 1 to 29)  
AUTHORS Stone,E.M., Sheffield,V. and Alward,W.L.M.  
TITLE Glaucoma-associated protein and corresponding nucleic acid and their therapeutic and diagnostic uses  
JOURNAL Patent: JP 2001503631-A 7 21-MAR-2001;  
COMMENT UNIVERSITY OF IOWA RESEARCH FOUNDATION  
OS Unidentified  
PN JP 2001503631-A/7  
PD 21-MAR-2001  
PF 07-NOV-1997 JP 1998521884  
PR 08-NOV-1996 US 08/748479,30-JAN-1997 US 08/791347 PR  
PI 21-MAR-1997 US 08/822959  
PI EDWIN M STONE,VAL SHEFFIELD,WALLACE L M ALWARD,PC  
CI2N15/12,C07K14/47,C07K16/18,A61K39/395,G01N33/53,C12Q1/68, PC  
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PC A61K31/70,A01K67/027  
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CC Topology: Linear;  
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BD225254  
LOCUS BD225254 29 bp DNA linear PAT 17-JUL-2003  
DEFINITION Remedies and diagnostic agents of glaucoma.  
ACCESSION BD225254  
VERSION BD225254.1 GI:33035024  
KEYWORDS JP 2002510508-A/9.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

REFERENCE 1 (bases 1 to 29)  
 AUTHORS Stone,E.M., Sheffield,V.C., Alward,W.L.M. and Fingert,J.  
 TITLE Remedies and diagnostic agents of glaucoma  
 JOURNAL Patent: JP 2002510508-A 9 09-APR-2002;  
 THE UNIVERSITY OF IOWA RESEARCH FOUNDATION  
 COMMENT OS Homo sapiens (human)  
 PN JP 2002510508-A/9  
 PD 09-APR-2002  
 PF 07-APR-1999 JP 2000542490  
 PR 07-APR-1998 US 09/056285  
 PI EDWIN M STONE, VAL C SHEPHERD, WALLACE L M ALWARD, JOHN FINGERT  
 PC C12N15/09, C12Q1/68, C12N15/00  
 CC Remedies and diagnostic agents of glaucoma  
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 LOCUS 131539 28 bp DNA linear PAT 06-FEB-1997  
 DEFINITION Sequence 451 from patent US 5582979.  
 ACCESSION 131539  
 VERSION 131539.1 GI:1822330  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 28)  
 AUTHORS Weber,J.L.  
 TITLE Length polymorphisms in (dc-da). sub.n. (dc-dt). sub.n sequences and method of using the same  
 JOURNAL Patent: US 5582979-A 451 10-DEC-1996;  
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 LOCUS AR051255 27 bp DNA linear PAT 29-SEP-1999  
 DEFINITION Sequence 23 from patent US 5830658.  
 ACCESSION AR051255  
 VERSION AR051255.1 GI:5974619  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 27)  
 AUTHORS Grayzov,S.M.  
 TITLE Convergent synthesis of branched and multiply connected

JOURNAL macromolecular structures  
 PATENT: US 5830658-A 23 03-NOV-1998;  
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 DB 27 GTGTGTGTGTGTGTGTGTGTGTGTGTGT 1

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 LOCUS AR127802 27 bp DNA linear PAT 16-MAY-2001  
 DEFINITION Sequence 23 from patent US 6180777.  
 ACCESSION AR127802  
 VERSION AR127802.1 GI:14114397  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 27)  
 AUTHORS Horn,T.  
 TITLE Synthesis of branched nucleic acids  
 JOURNAL Patent: US 6180777-A 23 30-JAN-2001;  
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 DEFINITION Sequence 23 from patent US 5571677.  
 ACCESSION 128384  
 VERSION 128384.1 GI:1819160  
 KEYWORDS  
 SOURCE Unknown.  
 ORGANISM Unclassified.  
 REFERENCE 1 (bases 1 to 27)  
 AUTHORS Grayzov,S.M.  
 TITLE Convergent synthesis of branched and multiply connected macromolecular structures  
 JOURNAL Patent: US 5571677-A 23 05-NOV-1996;  
 FEATURES Location/Qualifiers  
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ACCESSION 131231  
VERSION 131231.1 GI:1822022  
KEYWORDS  
SOURCE Unknown.  
ORGANISM Unclassified.  
REFERENCE 1 (bases 1 to 27)  
AUTHORS Weber, J.L.  
TITLE Length polymorphisms in (dc-da).sub.n.(dg-dt).sub.n sequences and method of using the same  
JOURNAL Patent: US 5582979-A 143 10-DEC-1996;  
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LOCUS AX175237 27 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 1 from Patent WO0144465.  
ACCESSION AX175237  
VERSION AX175237.1 GI:14596605  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Phillips, N.C. and Pillion, M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 1 21-JUN-2001;  
Bioniche Life Sciences Inc. (CA)  
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LOCUS AX175241 27 bp DNA linear PAT 03-JUL-2001  
DEFINITION Sequence 5 from Patent WO0144465.  
ACCESSION AX175241  
VERSION AX175241.1 GI:14598609  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Phillips, N.C. and Pillion, M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 5 21-JUN-2001;

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DEFINITION Sequence 66 from Patent WO0144465.  
ACCESSION AX175302  
VERSION AX175302.1 GI:14598670  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Phillips, N.C. and Pillion, M.C.  
TITLE Therapeutically useful synthetic oligonucleotides  
JOURNAL Patent: WO 0144465-A 66 21-JUN-2001;  
Bioniche Life Sciences Inc. (CA)  
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Db 1 GTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 27  
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ACCESSION AX189457  
VERSION AX189457.1 GI:15142969  
KEYWORDS  
SOURCE synthetic construct  
ORGANISM synthetic construct  
REFERENCE 1  
AUTHORS Phillips, N.C. and Pillion, M.C.  
TITLE Hyaluronic acid in the treatment of cancer  
JOURNAL Patent: WO 0147561-A 2 05-JUL-2001;  
Bioniche Life Sciences Inc. (CA)  
FEATURES  
Source  
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[illegible]

LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
BD176940/c	Gene related to open-angle glaucoma including normal tension glaucoma.	BD176940	1	GI:30014199	JP 2002306165-A/4.		1 (bases 1 to 25)	Hattori,Y. and Suzuki,R.	Gene related to open-angle glaucoma including normal tension	Patent: JP 2002306165-A 4 22-OCT-2002;	TSUBOTA LTD YUKIO HATTORI,RYO SUZUKI	OS Artificial sequence PN JP 2002306165-A/4 PD 22-OCT-2002 PI 17-MAY-2000 JP 2000144492 PI YUKIO HATTORI,RYO SUZUKI PC C12N15/09,C12Q1/68,C12N15/00 CC primer FH Key
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BD176940	Gene related to open-angle glaucoma including normal tension glaucoma.	BD176940	1	GI:30014199	JP 2002306165-A/4.		1 (bases 1 to 25)	Hattori,Y. and Suzuki,R.	Gene related to open-angle glaucoma including normal tension	Patent: JP 2002306165-A 4 22-OCT-2002;	TSUBOTA LTD YUKIO HATTORI,RYO SUZUKI	OS Artificial sequence PN JP 2002306165-A/4 PD 22-OCT-2002 PI 17-MAY-2000 JP 2000144492 PI YUKIO HATTORI,RYO SUZUKI PC C12N15/09,C12Q1/68,C12N15/00 CC primer FH Key
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BD176940	Gene related to open-angle glaucoma including normal tension glaucoma.	BD176940	1	GI:30014199	JP 2002306165-A/4.		1 (bases 1 to 24)	Weber,J.L.	Length polymorphisms in (dc-da).sub.n.(dc-dt).sub.n sequences and method of using the same	Patent: US 5582979-A 445 10-DEC-1996;	Location/Qualifiers 1..24 /organism="unknown" /mol_type="unassigned DNA"	
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BD176940	Gene related to open-angle glaucoma including normal tension glaucoma.	BD176940	1	GI:30014199	JP 2002306165-A/4.		1 (bases 1 to 24)	Weber,J.L.	Length polymorphisms in (dc-da).sub.n.(dc-dt).sub.n sequences and method of using the same	Patent: US 5582979-A 445 10-DEC-1996;	Location/Qualifiers 1..24 /organism="unknown" /mol_type="unassigned DNA"	
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LOCUS	DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT	FEATURES
BD176940	Gene related to open-angle glaucoma including normal tension glaucoma.	BD176940	1	GI:30014199	JP 2002306165-A/4.		1 (bases 1 to 24)	Weber,J.L.	Length polymorphisms in (dc-da).sub.n.(dc-dt).sub.n sequences and method of using the same	Patent: US 5582979-A 445 10-DEC-1996;	Location/Qualifiers 1..24 /organism="unknown" /mol_type="unassigned DNA"	
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